STIC-Biotech/ChemLib Slobodyansky, Elizabeth Tuesday, November 27, 2001 7:01 PM STIC-Biotech/ChemLib 09/590,375

Please search for case 09/590,375:

SEQ ID NOs: 1 and 2 against protein, DNA and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD Primary Examiner

AU 1652 CM1-10D11 tel. 306-3222

mail box 10C01

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: _///30/01 Searcher Prep/Review:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)
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Questel/Orbit: _	
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TAGE BLANK (USPTO)

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                              roAlaTrpLysGlyThrSerGlnAsnAspValGlyTyrGlyAlaTyrAsp 62
                          GlyThrGluMetValAsnAlaValGluValAsnArgSerAsnArgAsnGl 129
                                                                                                            lyIleGlnValTyrGlyAspValValMetAsnHisLysGlyGlyAlaAsp 112
                                                                                                                                                      CGGTTCAAAAGATGACCTAAAGTCACTAATTGCAGCTTTCAAAGATAAAG
                                                                                                                                                                                            {\tt rGlyThrArgSerGlnLeuGlnGlyAlaValThrSerLeuLysAsnAsnG}
                                                                      GAATCAATTGTCTAGCTGACATAGTGATCAACCAT.....
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(bases 1 to 665)

Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Center for Medicago Genomics Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2510 Sam Noble Parkway, Ardmore, OK 73402, Tel: 580 221 7302 Fax: 580 221 7380 Email. **-3'
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Ratio:
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Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: radixon@noble.org
Insert Length: 665 Std Error: 0.00
Plate: 047 row: G column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
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/tissue_type="Cell suspensions were subcultured every 14
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
days. Cells were induced with yeast
/note="Weetor: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
4 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
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/db_xref="taxon:3880"
/clone="NF047G02EC"
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1.594
50.800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 ValIleAsnGluLeuArgAsnTrpGlyValTrpTyrThrAsnThrLeuAs 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 AspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAsnLysIleTyrLy 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAA.....ATTTATATGGAAAATACTTCG.....CCANATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nLeuAspGlyPheArgIleAspAlaValLysHisIleLysTyrSerTyrT 246
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Anopheles gambiae GSS T7 end of clone 26N13 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                  This clone is from an A. gambiae BAC library provided by F.H Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                        Roux, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                              Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 681)
                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1
                          147
                                         /clone_lib="NotreDame1"
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/strain="PEST"
                                                                                         /db_xref="taxon:7165"
/clone="26N13"
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                   182 g
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alignment_block:
US-09-590-375-2 x CNS0100L/rev
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LOCUS AQ159867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 ACCTGTG.CTGCCGCCTGCCTACAAGGGCGCTTCCGGCGGCTACTCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 GCAGGAGGCCGCCGAGCGCCCCGCACCTGGCCGAACTGGGCATTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 ACCCTGCTGCAATTCTTCCACTGGTACTACCCCGACGGCGGCAAACTGTG
                                        source
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                                                                                                                                                                                                                                 Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                           Magnaporthe
                                                                                              Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson University, Clemson,
                                                                                                                                                                                                                                                                        Unpublished (1998)
                                                                                                                                                                                                                                                                                                          Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.

BAC End Sequencing Framework to Sequence the Magnaporthe gri
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 694)
                                                                                                                                                                                                                                                                                                                                                                                                                           Magnaporthe grisea.
Magnaporthe grisea
                                                                                                                                                       Tel: 864 656 5737 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ159867.1 GI:3556856
                                                                          High quality sequence stop: 452
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2.664
74.510
/organism="Magnaporthe grisea"
/strain="70-15"
                                                        Location/Qualifiers
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seq_documentation_block:
                                                                           seq_name: gb_est2:BG581061
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/note="Vector: pBACWICH; Site_2: HindIII; Site_2: HindIII;
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: 
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alTrpIleProProAlaTrpLysGlyThrSerGlnAsnAspValGlyTyr 58
                                                                                                            CTCTTTGAAGAACCTCATTCCTGACCTAGCAAATGCTGGAATTACACATG
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University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
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EST482791 GVN Medicago truncatula cDNA clone pGVN-63M12 5' end,
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Unpublished (2001)
Contact: Carroll P. Vance
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University of Minnesota name: M382117e TIGR sequence name:
MTCDD78TK More information is available at: http://www.mec
Seq primer: SKmod (CTA 9AA CTA 9t9 9AT CC).
Location/Qualifiers
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/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/hab_hosf="E. coli strain XLOLR"
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/db_xref="taxon:3880"
/clone="corrections"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lArgThrLysTyrGlyThrArgSerGlnLeuGlnGlyAlaValThrSerL 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spIleGluAsnGlyAsnTyrAspTyrLeuMetTyrAlaAspIleAspMet 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GATTGGGGCCCATCTTTCATTTGCAAAGA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HF037944 587 bp mRNA EST 19-DEC-2000 MF041C08FL1F1056 Phosphate starved leaf Medicago truncatula cDNA clone NF041C08PL 5', mRNA sequence.
BF637944
                                                                                            Plant Biology Division
The Samuel Roberts Nob
                                                                                                                                                           Medicago truncatula phosphate-starved leaf library Unpublished (2000)
                                                                                                                                                                                                      Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flore,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula
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                                                                                                                                       Contact: Harrison MJ
                                                                                                                                                                                                                                                                                                       Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                     barrel medic.
                                                                                                                                                                                                                                                                             (bases 1 to 587)
mjharrison@noble.org
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                                                                 Noble Parkway,
                                                                 Roberts Noble Foundation
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175 nLysIleTyrLysPheArgGlyThrGlyLysAlaTrpAspTrpGluValA
                                                                                                                                                                                                                                                                                                     125 rAsnArgAsnGlnGluIleSerGlyGluTyrThrIleGluAlaTrpThrL 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 CTCTTTCAGGGATTCAACTGGGAGTCAAGTAACAAAGGAGGATGGTACAA
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                                                                                                                                                                                               ysPheAspPheProGlyArgGlyAsnThrHisSerAsnPheLysTrpArg 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAAGATAAAGGAATCAATTGTCTAGCTGACATAGTGATCAACCAT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euLysAsnAsnGlyIleGlnValTyrGlyAspValValMetAsnH1sLys 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .GCATCAAAATACGGTTCAAAAGATGACCTAAAGTCACTAATTGCAGCTT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alTrpIleProProAlaTrpLysGlyThrSerGlnAsnAspValGlyTyr 58
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                                                 .....GATTGGGGCCCATCTTTCATTTGCAAAGA 426
                                                                                                TrpTyrHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGlnAs 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Phosphate starved leaf"
/tissue_type="leaf"
/dev_stage="trifoliate"
/dev_stage="trifoliate"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
/runcatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
a 117 c 119 g 179 t
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/db_xref="taxon:3880"
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Gaps: 8
Percent Identity: 26.316
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KEYWORDS
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VERSION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BF632036
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US-09-590-375-2 x BF632036
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76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspHisProGluValIleAsnGluLeuArgAsnTrpGlyValTrpTyrTh 225
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                                 9 MetMetGlnTyrPheGluTrpHisLeuProAsnAspGlyAsnHisTrpAs 25
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  ::::::|| | |||:::|||:::
CTCTTTCAGGGATTCAACTGGGAGTCAAGTAACAAAGGAGGATGGTACAA 125
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NF016C06DT1F1039 Drought Medicago truncatula cDNA clone NF016C06DT
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   barrel medic. Medicago truncatula Medicago truncatula Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: gdmay@noble.org
Insert Length: 639 Std Error: 0.00
Plate: 016 row: C column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Plantlets"
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/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                  timepoints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Drought"
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                                                                                                                                                                            196.00
1.607
50.833
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Gaps: 9
Percent Identity: 27.083
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ACCESSION
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LOCUS BF647599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 TGACACTGCTTATTCAGATGGCACTGGA......A 472
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                                       Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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131 eSerGlyGluTyrThrIleGluAlaTrpThrLysPheAspPheProGlyA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 AAAAGATGACCTAAAGTCACTAATTGCAGCTTTCAAAGATAAAGGAATCA 314
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                                                                                                                                                                                                                                                                                                                                         98 lnValTyrGlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThr 114 
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                                                                                              .....AGAACAGCAGAAAAGAAAGATGA 366
                                                                                                                                                                                   GluMetValAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIl 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspLeuGlyGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyTh 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpLysGlyThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyr 64
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7302
Fax: 580 221 7380
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Insert Length: 635 Std Error: 0.00
Plate: 077 row: E column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.
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129 c 125 g 197 t 1 others
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/db_xref="taxon:3880"
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Fax: (51 Email: m Seq prin High qua FEATURES Source	TION ION ION ORS E E NISM NALL TION TION TION TION TION TION TION TION	367 TAGAGGCATCTA 148 rgGlyAsnThrH ::: 395GGGACTCCTG 165 ThrAspTrpAsp 416GATTGGGGC 181 gGlyThrGlyLy 463 TGGCACTGGA 198 yrAspTyrLeuM 191GGCTATCAAG 215 ASNGLULEUATG ::: 539 AAAGAGTTATCT
Fax: (517)-337-6782 Email: mitchmcg@pilot.msu.edu Seq primer: T3 Location/Qualifiers 1771 /organism="Beta vulgaris" /cultivar="USH20" /db_xref="taxon:161934" /clone="ys016f79" /clone="isougar Beet germination cDNA library" /tissue_type="whole seedlings" /dev_stage="4-day germination under stress (salt/NaCl, dehydration/Mannitol and anaerobic stress)" /lab_host="SOLR" /notc="Organ: seeds; Vector: pBluescript II KS (+) excised from Lambda Uni-Zap XR; Site_1: EcoRI; Site_2: XhoI; cDNAs were derived from reverse transcription of pooled mRNA samples from stressed seedlings (germinated for 4 days in 150mM NaCl, 200mM Mannitol, submerged in distilled water and 0.3% Hydrogen peroxide). The cDNA library was	TTGTCAAANGTTATGCGCCTAGCATAACA EST et germination cDNA library Be milar to alpha amylase, mRNA s:10711301 idiplantae; Streptophyta; Embr Magnollophyta; eudicotyledons; Caryophyllales; Chenopodiace 771) G. McGrath.J.M., Myers,S. ar ene expression in sugar beet s onder stress conditions 000) tchell McGrath etics Lab., USDA/ARS/Sugar Bee University Soil Sci. Bldg., East Lansing	TAGAGGCATCTATTGCCTCTTTGAAGGT. 394 rgGlyAsnThrHisSerAsnPheLySTrpArgTrpTyrHisPheAspGly 164 :::

generated by directional ligation of the cDNAs

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                            nTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheArgIleA 236
                                                                                                                                                                   luValAspIleGluAsnGlyAsnTyrAsp......TyrLeuMet 202
                                                                                                                                                                                                                                                  uGlnAsnLysIleTyrLysPheArgGlyThrGlyLysAlaTrpAspTrpG 190
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                                                                     GCACCTGATATAGACCATCTTAATCCAAGAGTACAAAAGGAGTTAGTCGA
                                                                                                   TyralaaspIleaspMetaspHisProGluValIleasnGluLeuargAs
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                                                                                                                                                                                                                                                                                                                          TrpArgTrpTyrHisPheAspGlyThrAspTrpAspGlnSerArgGlnLe 173
TTGGATGAATNGGCTCAAGACAGAAATTGGTTTTGACGGATGGAGATTTG
                                                                                                                                              AATACTCTGATGGTAGTGGAAATCTAGACACTGGAGCTGGTTATGGTGCT
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144 c 178 g 224 t 2 others
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                                             alignment_block:
US-09-590-375-2 x AQ159694
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Align seg 1/1
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1 (bases 1 to 743)

Yu, Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.

BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnaporthe grisea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 864 656 5737 Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                               Quality:
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100 Jordan Hall, Clemson Universiy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lone mgxb0001108r, DNA sequence
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to: AQ159694
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                                                                                                                                                                                                                                                                            numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."

5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
/lab_host="E. coli DH10B"
/note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
/note="Vector: pBACWICH; Site_1: HindIII; fungal diseases
Rice blast is one of the most devestating fungal diseases
of rice world wide. It is a filamentous ascomycete with
a haploid genome (n=7) of approximately 40 Mbp. Rice
blast is an important model fungal pathogen for studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Magnaporthe grisea"
/strain="70-15"
                                                                                                                    190.50
2.721
61.947
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/clone_lib="CUGI Rice Blast BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                     494 Plant and Soil Sci. Bldg.,
Tel: (517)-432-2355
Fax: (517)-337-6782
Email: mitchncg@pllot.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: J. Mitchell McGrath
Sugar Beet Genetics Lab., USI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
1 (bases 1 to 702)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michigan State University
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                                                                                                                                                                                                                                                                                                                                                                primer: T
                                                                                                                                                       /clone_lib="Sugar Beet germination cDNA library"
/tissue_type="whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl,
dehydration/Mannitol and anaerobic stress)"
/note="Organ: seeds; Vector: pBluescript II KS (+) excised from Lambda Uni-Zap XR; Site_1: EcoRI; Site_2: KhOI; cDNAs were derived from reverse transcription of pooled mRNA samples from stressed seedlings (germinated for 4 days in 150mM NaCl, 200mM Mannitol, submerged in distilled water and 0.3% Hydrogen peroxide). The cDNA library was
                                                                                                                                                                                                                                                /db_xref="taxon:161934"
                                                                                                                                                                                                                                                                         /cultivar="USH20"
                                                                                                                                                                                                                                                                                            /organism="Beta vulgaris"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                    'lab_host="SOLR"
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alignment_block:
US-09-590-375-2 x BI073204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 TAATTCACTGAAAAACTCAATCGATGATTTGGCTAGAGCAGGGGTTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 TTGTTTCAGGGTTTCAATTGGGAATCATGCAACAAACCAGGAGGATTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 pAsnArgLeuArgAspAspAlaAlaAsnLeuLysSerLysGlyIleThrA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 MetMetGlnTyrPheGluTrpHisLeuProAsn...AspGlyAsnHisTr
                                                                                        AlaAspIleAspMetAspHisProGluValIleAsnGluLeuArgAsnTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rValArgThrLysTyrGlyThrArgSerGlnLeuGlnGlyAlaValThrS
             pGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheArgIleAspA
                                                                                                                                                               alAspIleGluAsnGlyAsnTyrAsp.....TyrLeuMetTyr
                                                                                                                                                                                                                                       nAsnLysIleTyrLysPheArgGlyThrGlyLysAlaTrpAspTrpGluV 191
                                                                                                                                                                                                                                                                                                                    ArgTrpTyrHisPheAspGlyThrAspTrpAspGlnSerArgGlnLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gSerAsnArgAsnGlnGluIleSerGlyGluTyrThrIleGluAlaTrpT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysGlyGlyAlaAspGlyThrGluMetValAsnAlaValGluValAsnAr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTCCACCAAAAAGGAATCAAATGTGTTGCGGATATAGTGATAAATCAT
                                                       CCCGATATAGACCATCTAAATCCAAGGGTACAAAGAGAACTAGTTGATTG
                                                                                                                               ACTCTGACGGTAGTGGAAATCTAGACACTGGAGCTAGTTATGGTGTCGCA
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128 c 167 g 201 t 1 others
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LOCUS BE922066
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                                         116
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                                                                                                                                                                                                      16 ACATCAGGAACTGGTACAGGATTTGAGATTTTGTGCCAGGGTTTTAATTG
  49
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                                                                                                                                                                                                                                         5 ThrAsnGlyThr......MetMetGlnTyrPheGluTr 15
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{\tt LysGlyThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAs}
                                         CGGAGTTATCTTCACTTGGATTCAGTGTGATCTGGTTACCTCCACCAACT 165
                                                                           laAsnLeuLysSerLysGlyIleThrAlaValTrpIleProProAlaTrp
                                                                                                                      GGAATCTCATAAATCTGGAAGATGGTACAAGGAGCTACATGAAAAAGCTG
                                                                                                                                                         pHisLeuProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaA 32
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1 (bases 1 to 515)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J., Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning, C.M., Fry, W.E., Tanksley, S.D. and Baker, B. Generation of ESTs from potato leaves and petioles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE922066 515 bp mRNA EST
EST425835 potato leaves and petioles Solanum
CSTB17J6 5' sequence, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Ronning
The Institute for Genomic Research
For clone request: please contact Research Genetics,
pivision tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Solanum tuberosum"
/cultivar="Kennebec"
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1.509
51.542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 GGAGATAATTTCCATGCTGCTCCTAACATTGATCATTCCCCAGGAATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 lyThrGlyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyr 198
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                                                                                                                                                                                       1 (bases 1 to 678)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST300357 tomato fruit red rip
clone cLEN12E8, mRNA sequence.
                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum Eukaryota; Uridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Spermatophyta; Magnoliophyta; Eukaryota; Solanaceae; Solanum; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                             tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                AW223546.1 GI:6535230
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                                                                                                                                   Clemson University Genomics Institute
                                                                                                                                                      Contact: CUGI
                                                                                                                                                                      Unpublished (1999)
                                                       sequence.
organism="Lycopersicon esculentum"/
                                   Location/Qualifiers
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...GAAGCAACTGAACCTTACTTCGCTGTAGGCGAGTTTTGGGATTCCCCT 186
GATGCAAGGTTATGCCTATATCCTGACT...CACCCTGGAACCCCGTCAG
                                                                                                                                                              GluAlaLeuGluSerPheValGlnSerTrpPheLysPro...... 350
                                                                                                                                                                                                                    GGCCATCTCGTGCTGTTACATTTATAGAGAATCATGATACAGGTTCTACA 433
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                                                                                                                                                                                                                                                                                                                                                                                e.....AspMetArgAsnIleLeuAsnGlySerValValGlnLysH 321
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGACAACGAAGGGAATTCTTCATTCTGCAATTGAGAGATGTGAATACTG
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                                                ....LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerV 366
                                                                                                                                                                                                                                                                       isProIleHisAlaValThrPheValAspAsnHisAspSerGlnProGly 337
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/note="Vector: pBlueScript SK(-); Site_1: Econt; Site_2:
xhol; supplier: Glovannoni; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe), 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
a 118 c 183 g 194 t
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/tissue_type="pericarp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cLEN12E8"
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SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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ORIGIN
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  seq_name:
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Quality:
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                                          409
                                                                                                                          359
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                                     GAGCCCGGTTATGCTGTATATGACCTGTACGATCTGGGCGAATTTGAT
                                                               AspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsn 70
                                                                                                                          TTACCCATGTTTGGCTCCCACCGGCTTATAAGTCAGCCTTTGGCACAGAG
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gb_est1:AW709933
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Arabidopsis thaliana genome survey sequence SP6 end of BAC T7A19 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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AL091025
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/clone="T7A19"
/note="end : SP6"
a 112 c 88 g
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3.402
77.273
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/strain="Columbia"
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243 TyrSerlyr:	alignment_block: US-09-590-375-2 x Align seg 1/1 to:	alignment_scores: Quality: Ratio: Percent Similarity:	ACCESSION AW709933 ACCESSION AW709933.1 GI KEYWORDS EST. SOURCE Neurospora cras CORGANISM EUArryota; Funa I (bases 1 to Contact: Bruce Department of Advanced Cente 620 Parrington Tel: 405 325 4 Fax: 405 325 7 Fax: 405 325 7 Fax: 405 325 1 Email: broe@ou We anticipate Genetics Stock Seq primer: Un High quality st Source //clor //tiss dark //nott ECORN BASE COUNT B2 a 1	seq_documentation_block: LOCUS AW709933 DEFINITION d9b06ne.fl N cDNA clone d
TyrSerTyrInratgaspiipheuilinins vai.	AW709933 : AW709933 from: 1 to: 436	7: 169.00 Length: 145 5: 2.036 Gaps: 4 7: 57.241 Percent Identity: 31.034	GI:7599010 Crassa. Crassa. Crassa. Fungi: Ascom Fungi: Ascom Fungi: Ascom Fungi: Ascom Fungi: Ascom Fungi: Ascom Gi Chemistr: Ascom Funce A. Roe. Of Chemistr: Ascom Funce A. Roe. Of Chemistr: Ascom Funce A. Roe. Of Chemistr: Cok Center Funce A. Roe. Of Chemistr: Ascom Gi Chemistr: Ascom Ascom Ascom Ascom Clone="dobolo Clone="funce" Clone Gi CDN Com	ock: 436 bp mrNA EST 25-APR-2000 fl Neurospora crassa evening cDNA library Neurospora crassa ne d9b06ne 5', mRNA sequence.

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                                                                    MEDLINE=86008166; PubMed=3876333;
Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Ud
"Complete nucleotide sequence of a thermophilic alpha-amylase homology between prokaryotic and eukaryotic alpha-amylases at active sites.";
                                                                                                                                               J.
                                                                                                                                                                                                                                      Haris.
Bacillus stearothermophilus.
Bactería; Firmicutes; Bacillus/Clostridium
Bactería; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                  AMY_BACST STANDARD; PRT; 549 AA.
P06279; Q45519;
01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annoctation update)
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
          Gray
                                                                                                                                                                     gene
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MEDLINE-85234394; P
                                                                                                                                                                                                                                Bacillus/Staphylococcus
NCBI_TaxID=1422;
                     STRAIN=NZ-3;
MEDLINE=86195857; PubMed=3009417;
                                                                                                                           SEQUENCE FROM
STRAIN-DY5/PHI
                                                                                                                                                                             Nakajima R., Imanaka
"Nucleotide sequence
                                           SEQUENCE
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                                              MEDLINE-82051296; PubMed=6170539;
Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P. Soederlund H., Takkinen K., Kaeaeriaeinen L.;
Nucleotide sequence of the promoter and NH2-terminal region of the alpha-amylase gene from Bacillus amyloli
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MEDLINE=80241725; P
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Gene 59:161-170(1987).

-i- CATALYTIC ACTIVITY: ENDOHYDDOLYSIS OF 1,4-ALPHA-GLUCOSIDIC
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KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                        YPSVFYGDYYGIPTHG-----VPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREG
                                                                                                                        QGGGYDMRRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRESG
                                                                                                                                           SGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQG
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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I -> I (IN REF. 2).
S -> D (IN REF. 2).
G -> S (IN REF. 2).
G -> S (IN REF. 2).
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Title: Perfect score: US-09-590-375-2 2713 1 HHNGTNGTMMQYFE

Sequence: HHNGTNGTMMQYFEWHLPND.....ADGWGNFTVNGGAVSVWVKQ 485

Searched: 100059 seqs, 36664827 residues Gapop 10.0 , Gapext 0.5

Scoring table:

BLOSUM62

Total number of hits satisfying chosen parameters:

100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	<u> </u>	Result
255.5 253 249.5 247.5 246	Score 2410 1906 1906 1907 1053 1053 1053 1053 294 284 284 284 284 284 277 274 274 275 276 276 276 276 276 276 276 276 276 276	
9.2 9.1 1		Query
718 703 413 711 437	,	
CDGT_BACLI CDGT_BACS2 AMY3_WHEAT CDGT_BACST AM3E_ORYSA	AMT6_BACS7 AMY_BACLI AMY_BACST AMY_BACST AMY_BACST AMY_BACST AMYB_PAEPO AM3A_ORYSA AM74_PSEST AM75_BACCI CDGT_BACS9	
P14014 bacillus li P31746 bacillus sp P08117 triticum ae P31797 bacillus st P27934 oryza sativ	Description P19571 bacillus sp P06278 bacillus li P06279 bacillus st P006279 bacillus am P26613 salmonella P26613 salmonella P26613 salmonella P26613 salmonella P26614 paenibacill P27932 oryza sativ P17859 vigna mungo P13507 pseudomonas P22963 pseudomonas P22963 pseudomonas P23963 pseudomonas P23963 pseudomonas P23963 pseudomonas P23963 pseudomonas P317692 bacillus sp P08121 bacillus sp P08121 bacillus scillus scillus scillus scillus scillus sp P30921 bacillus scillus scill	

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Matches 419;

Conservative

88.8%; Score 2410; DB 1; Length 518; 86.4%; Pred. No. 4.7e-157; tive 36; Mismatches 30; Indels

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Gaps

0

Query Match Best Local Similarity

SEQUENCE

34 518 C 518 AA; 59009 MW;

GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
1; 3A961E21612682C4 CRC64;

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219	222	223.5	225	230.5	231	232.5	233.5	236.5	237.5	237.5	243
8.1	8.2	8.2	8.3	8.5	8.5	8.6	8.6	8.7	8.8	8.8	9.0
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P21567	086956	P80099	P04830	P30292	P19531	P27941	P10529	P27935	Q02906	Q02905	P31835
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P06278;
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WEDLINE-86111694; PubMed-2418011;
Yunki T., Nomura T., Tezuka H., Tsuboi A., Yamagata Yunki T., Nomura T., Tezuka H., Tsuboi A., Yamagata Tsukagoshi N., Udaka S.;
"Complete nucleotide sequence of a gene coding for pH-stable alpha-amylase of Bacilius licheniformis: pH-stable alpha-amylase of three bacterial liquefying deduced from the DNA sequences.";
J. Biochem. 98:1147-1156(1985).
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Bacillus licheniformis

Bacitlus/staphylococcus group;

Bacillus/Staphylococcus group;
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   SEQUENCE OF 1-104 FROM N.A.

MEDLINE=84185455; PubMed=6609154;

MEDLINE=84185455; PubMed=6609154;

MILLINE=84185455; PubMed=6609154;

MILLINE=8418545; PubMed=6609154;

MILLINE=841855; PubMed=6609154;

MILLINE=8418555; PubMed=6609154;

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Carmona C., Requadt
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                                                                                                                                                                                                                                    "Structural genes encoding the thermophilic alpha-amylases Bacillus stearothermophilus and Bacillus licheniformis."; J. Bacteriol. 166:635-643(1986).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=86195857; PubMed=3009417;
Gray G.L., Mainzer S.E., Rey M.W.,
Carmona C., Requadt C.;
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(Rel. 06, Last sequence update)
(Rel. 40, Last annotation update)
SE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
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PIR; B24549; B24549.

PIR; B26151; A26151.

PDB; 1US; 17-AUG-96.

PDB; 1US; 12-MAR-97.

InterPro; IPR000461; Alpha_amylase.

Pfam; PF00128; alpha-amylase; 1.
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EMBL; M38570; ÅAA22226.1; ...
EMBL; M13256; AAA22240.1; ...
EMBL; K01984; AAA22193.1; ...
EMBL; M26412; AAA22193.1; ...
EMBL; A17930; CAA01355.1; ...
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SEQUENCE OF 1-29 FROM N.A.
MEDLINE=89213924; PubMed=2540150;
Macconnell D.J.;
Macconnel
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"Crystal structure of calcium-depleted Bacillus licheniformis alpha-
anylase at 2.2-A resolution.";

J. Mol. Biol. 246:545-559(1995).

J. Mol. Biol. 246:545-559(1995).

I. CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC

INNEAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

INNEAGES IN OLIGOSACCHARIDES AND INDUSTRY FOR HIGH TEMPERATURE

ILIQUEFACTION OF STARCH-CONTAINING MASHES AND IN THE DETERGENT ILIQUEFACTION OF STARCH-CONTAINING MASHES AND IN THE DETERGENT INDUSTRY TO REMOVE STARCH. SOLD UNDER THE NAME TERMAMYL BY
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promoter-independent catabolite repression in
J. Bacteriol. 171:2435-2442(1989).
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J. Bacteriol. 149:372-373(1982).
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"N-terminal amino acid sequence of Bacillus licheniformis
alpha-amylase: comparison with Bacillus amyloliquefaciens
pacillus subtilis Enzymes.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
Q -> Y (IN REF.
R -> L (IN REF.
S -> G (IN REF.
S -> G (IN REF.
Score 1906; DB 1;
Pred. No. 9.6e-123;
7; Mismatches 73;
                                                                                                                                                                 Q -> Y (IN REF. 5).
S -> G (IN REF. 2).
A -> S (IN REF. 2).
D8BB77759CD4C482 C)
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R -> L (IN REF.
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                                                                                                                                                                                CRC64;
                                                                   Length 512;
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Query Match Best Local S Matches 335

Similarity

70.3%;

Conservative

67;

Indels

10;

Gaps

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18;

84; Mismatches 183; Indels

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207; Conservative
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                506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-6 FROM N.A.
STRAIN-SYM1103;
MEDLINE-92407478; PubMed-1527488;
MEDLINE-92407478; PubMed-1527488;
Rawaqishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
"Subdivision of flagellar region III of the Escherichia coli and Salmonella typhimurium chromosomes and identification of two additional flagellar genes";
J. Gen. Microbiol. 138:1051-1065(1992).
SEQUENCE OF 476-494 FROM N.A.

SABA M., Kihara M., Kawagishi I., Macnab R.M.;

Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC

LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

-!- SUBCLIULAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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"Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
J. Bacteriol. 174:6644-6652(1992).
                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
CYTOPLASMIC ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
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4FA6BDBFEDD5E47C CRC64;
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SLYGENE; SG10011; amyA.
A InterPro; IPR000461; Alpha_amylase.
R Pfam; PF00128; alpha amylase; 1.
R Pfam; PF00128; alpha amylase; 1.
W Hydrolase; Glycosidase; Carbohydrate metabolism.
W Hydrolase; Glycosidase; Carbohydrate metabolism.
W ACT_SITE 235 235 BY SIMILARITY.
T ACT_SITE 239 239 BY SIMILARITY.
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                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
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SVSIYVQK 514
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AMY 2_SALTY
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Length 494;

Score 1053; DB 1; Pred. No. 1.1e-64;

38.8%;

Query Match Best Local Similarity

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                                                                                                                                                                     DLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 124
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STRAINFALZ / MG1657.
STRAINFALZ / MG1657.
PUDMEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                            302 QGAEYDMRHIFTGTLVEADPFHAVTLVANHDTQPLQALEAPVEPWFKPLAYALILLRENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||| | || :|| :|| :| || 362 VPSVFYPDLYGASYEDSGENGETCRVDMPVI-NQLDRLILARQRFAHGIQTLFFDHPNCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 YSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASN
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"Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
J. Bacteriol. 174:6644-6652(1992).
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Escherichia coli
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63 DLGEFDQKGSIPTKYGDKAQLLAAIDALKRNDIAVLLDVVVNHKMGADEKEAIRVQRVNA 122
                                                                                              183 IGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIK
                                125 SNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRG--
                                                     STANDARD;
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1. yoosidase; Carbohydrate metabolism; Complete proteome. 235 235 BY SIMILARITY.
239 239 BY SIMILARITY.
332 BY SIMILARITY.
332 BY SIMILARITY.
340 109 A -> V (IN REF. 1).
351 109 109 A -> V (IN REF. 1).
352 234 L.-> I (IN REF. 1).
353 234 L.-> I (IN REF. 1).
354 56539 MW; 26AFF6797DDA54D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       large non-coding region.";
J. Gen. Microbiol. 139:1401-1407(1993).
-!- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
-!- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     Raha M., Kihara M., Kawagishi I., Macnab R.M.; "Organization of the Escherichia coli and Salmonella typhimurium chromosomes between flagellar regions IIIa and IIIb, including a
                                                                                                                                                                                                                                     Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.P. Subdivision of flagellar region II of the Escherichia coli and Salmonella typhimurium chromosomes and identification of two additional flagellar genes.";
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                                                             χ.
          MEDLINE-97251358; PubMed-9097040; Itch T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kinura S., Kitakwa M., Kitagawa M., Mitagawa M., Mizobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.; A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 401-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 495;
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Pred. No. 1.4e-62;
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HSSP; P06278; 1BPL.
ECOGENE; E011387; amyA.
Interpro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase.
Hydrolase; Glycosidase; Carbohydrate
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EMBL; AE000285; AAC74994.1; -.
EMBL; D90833; BAA15755.1; -.
EMBL; M85240; -; NOT_ANNOTATED_CDS.
EMBL; L13279; AAA82575.1; -.
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                                                                                                                                                                                               SEQUENCE OF 1-5 FROM N.A.
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DLGEFNQKGTVRTKYGTRSOLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 124

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Kawazu T., Nakanishi Y., Dozumi N., Sasaki T., Yamagata H., Tsukagoshi N., Udaka S.; "Cloning and nucleotide sequence of the gene coding for enzymatically active fragments of the Bacillus polymyxa beta-amylase."; J. Bacteriol. 169:1564-1570(1987).
                                                                                                                                                    363 YPSVFYGDYYGIPTHGVPS-------MKSKIDPLLQARQTYAYGTQHDYFDHHDIIG 412
                                                                                                                                                                                                                                                                                                                                                                    WIREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNF 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 YSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASN 302
                                                  242 AWFYKEWIEHVQEVAPKPLFIVAEYWSHEVDKLQTYIDQVEGKTMLFDAPLQMKFHEASR 301
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1999 (Rel. 18, Last annotation update)
BETA/ALPHA-AMYLASE (EC 3.2.1.1);
ALPHA-AMYLASE (EC 3.2.1.1)!
Pachibacillus polymyxa (Bacillus polymyxa).
Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Paenibacillus.
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MEDLINE-87231094; PubMed=2438660;
MEDLINE-87231094; PubMed=2438660;
MEDLINE-87231094; PubMed=2438660;
MENOdes C., Strasser J., Friedberg F.;
"Sequence of a maylase.";
Nucleic Acids Res. 15:3934-3934(1987).
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Uozumi N., Matsuda T., Tsukagoshi N., Udaka S.;.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINES.
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AMYB_DAMYB_DA
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DT 01-MAX
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DD 01-MAX
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                                                                                                                                                         CATALYTIC ACTIVITY: HYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN POLYSACCHARIDES SO AS TO REMOVE SUCCESSIVE MALTOSE UNITS FROM THE NON-REDUCING ENDS OF THE CHAINS.
                      polymyxa beta-amylase.";
Biochmistry 30:4594-4599(1991).
-!- FUNCTION: THE PRECUESOR PROTEIN IS PROTEOLITICALLY CLEAVED TO
PRODUCE MULTIFORM BETA-AMYLASES AND A 48 KDA ALPHA-AMYLASE AFTER
                                                                                                                                                                                                                                  -: CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1.4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYASACCHARIDES.
-: SUBCELLULAR LOCATION: SECRETED.
-: SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO FAMILY 14 OF GLYCOSYL HYDROLASES (BETA-AMYLASES).
-: SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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C-N: 20 FOLD DECREASE IN ACTIVITY.

C-SS: 60 FOLD DECREASE IN ACTIVITY.

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N -> D (IN REF. 3).

S -> D (IN REF. 3).

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"Structural and functional roles of cysteine residues of Bacillus
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InterPro; IPR001554; Glyco_hydro_14.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF001373; Glyco_hydro_14; 1.
Pfam; PF00150; BETAANYLASE;
PRINTS; PR00841; GLHYDLASE14A.
PROSITE; PS00506; BETA_AMYLASE_1; 1.
PROSITE; PS00509; BETA_AMYLASE_2; 1.
Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
Polysaccharide degradation; Repeat.
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SUBUNIT: MONOMER.

TISSUE SPECIFICITY: MOST ABUNDANT IN EMBRYO-DERIVED CALLUS TISSUE.
DEVELOPMENTAL STAGE: EXPRESSED AT A HIGH LEVEL DURING GERMINATION IN THE ALEURONES CELLES UNDER THE CONTROL OF THE PLANT HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 NLYNASNSGCYFDMRNILNGSVVQKHPIHAVT---FVDNHD-----SQPGEALESF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            991
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                                                                                                                                                                                                                                                                                                                                                                                                             60 AYDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 VEVNRSNRNQEISGEYTIEAWTKFDF-PGRGNTHSNF-KWRWYHFDG--TDWDQSRQLQN 175
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                      1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDV-GYG 59
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1998 (Rel. 37, Last annotation update)
ALPDEC.1998 (Rel. 37, Last annotation update)
ALPHA-AMYLASE ISOZYME 3A PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
AMY1.2 OR AMY3A.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.; "Characterization of an alpha-amylase multigene cluster in rice."; Plant Mol. Biol. 16:579-591(1991).
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-1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
                                                                                                           138;
; DB 1; Length 1196; 5.5e-14;
                                                                                                67; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CV. JAPONICA M202; TISSUE=Etiolated leaf;
MEDLINE=91329692; PubMed=1714318;
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11.6%; Score 315; 24.1%; Pred. No. 5
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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01-MG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
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56; Mismatches
                                                                                 KNOWN AS THE ALPHA-AMYLASE FAMILY.
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
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MEDLINE=94120017; PubMed=8290640;
Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
Wocdechide sequence of the alpha-amylase gene from Vigna mungo.";
Plant Physiol. 103:1459-1459(1993).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1.4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
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EMBL, X73301; CAA51734.1; -
PIR; S10514; S10514.
PIR; S40201; S40201.
MARSP, P04063; 1AMY.
Mendel; 12451, VIGML; Amyl; 1.
InterPro; IPR000461; Alpha_amylase.
Pfam; PF00128; alpha-amylase; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
SIGNAL.
1 33 PROBABLE.
                                                                                                                                                                                                                              Yamauchi D., Minamikawa T.;
Yamauchi D., Minamikawa T.;
"Nucleotide sequence of cDNA for alpha-amylase from cotyledons of germinating Vigna mungo seeds.";
Nucleic Acids Res. 18:4250-4250(1990).
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MEDLINE=90332425; PubMed=2377468;
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Hasegawa K., Kubota M., Matsuura Y.;
"Roles of catalytic residues in alpha-amylases as evidenced by the
structures of the product-complexed mutants of a maltotetraose-forming
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
6LUCAN 1,4-ALPHA MALTOTETRAHYDROLASE PRECURSOR (EC 3.2.1.60) (G4-AMYLASE) (MALTOTETRAOHYDROLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujita M., Torigoe K., Nakada T., Tsusaki K., Kubota M., Sakai S., Tsujisaka Y.; Torigoe K., Nakada T., Tsusaki K., Kubota M., Sakai S., "Cloning and nucleotide sequence of the gene (amyP) for maltotetraose-forming amylase from Pseudomonas stutzeri MO-19."; J. Bacteriol. 171:1333-1339(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Crystal structure of a maltotetraose-forming exo-amylase from Pseudomonas stutzeri.";
J. Mol. Biol. 267:661-672(1997).
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Sakai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
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                                                                                                                                               313 TQRL-----WPFPSDKVMQGYAYILT-HPGTPSIFYDHFF 346
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                                                                                                         GEALESFVQSWFKP----LAYALILTREQGYPSVFYGDYY
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MEDLINE-97271999; PubMed-9126844;
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                  294 HYNLYNASNSGGYFDMRNILNGSV-
                                                                                                                                                                                                                                                                  STANDARD;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YGAYDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTE 115
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                                                                                                                                                                                                                                                       InterPro; IPR000461; Alpha_amylase.
InterPro; IPR0010461; Alpha_amylase.
InterPro; IPR001044; CBD_4.
Pfam; PF00128; alpha-amylase; 1.
Propon; PF001568; CBD_4; 1.
Probon; PF001568; CBD_4; 1.
Bydrolase; Glycosidase; Signal; Carbohydrate metabolism; Calcium;
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25.0%; Pred. No. 2.6e-12;
Live 65; Mismatches 168
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PDB; 1Q15; 24-NOV-99
PDB; 1QPK; 17-NOV-99
                                                                                                                            ; 2AMG; 01-APR-97
; 1JDA; 15-0CT-97
                                                                                                                                                                  1JDC; 15-OCT-97
1JDD; 15-OCT-97
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PDB; 2AMG; 01-APP-07
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                                                                                                                                                                                                                                                                                                                     QVRR--AAGVRAD-----SAISFH--SGYSGLVATVSGSQQTLVVALNSDLGN 414
                                                                                                                                                  01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 31, Last annotation update)
GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE PRECURSOR (EC 3.2.1.60) (G4-MALTAGE) (MALTOTETRAOSE-FORMING ANYLASE) (EXO-MALTOTETRAOHYDROLASE)
(MALTOTETRAOSE-FORMING EXO-AMYLASE).
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PTR. S05667; S05667.
HSSP, P13507; ZAMG.
InterPro: IPR0000461; Alpha_amylase.
InterPro: IPR0000461; Alpha_amylase.
Ffam; PF00128 alpha-amylase; 1.
Ffam; PF00186; CBD_4; 1.
PyrDom; PD001568; CBD_4; 1.
Hydrolase; Glycosidase; Signal; Carbohydrate metabolism; Calcium. SIGNAL
                       391 QARQTYAYGTQHDYFDHHDIIGWTREGDSSHPNSGLATIMSDGPGGNKWMYV-----
                                                                                                                                                                                                                                                                                       Zhou J., Baba T., Takano T., Kobayashi S., Arai Y.; "Nucleotide sequence of the maltotetraohydrolase gene from pseudomonas saccharophila.";
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NCBI_FaxID=304;
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MEDLINE=90005970; PubMed=2676600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 GKSGGGEGYFWHD-----FNKNG----RYGSDAQLRQAAGALGGAGVKVLYDVVPNH-- 138
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MEDLINE=90147765; PubMed=1689153;
Itkor P., Tsukagoshi N., Udaka S.;
Itkor P., Tsukagoshi N., Udaka S.;
"Nucleotide sequence of the raw-starch-digesting amylase gene from Bacillus sp. B1018 and its strong homology to the cyclodextrin glucanotransferase genes.';
glucanotransferase genes.',
e.chem. Biophys. Res. Commun. 166:630-636(1990).
Picker RAW STARCH.
DIGEST RAW STARCH.
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RAW-STARCH-DIGESTING AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GTSQNDVGYGAYDLYDLGEFNOKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::| ::| | |:: | | |:: | | |:: | |:| |:: |:| |:: |::| |:: |::| |:: |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
-!- SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                  153;
                                                                                                                                                                                                                                                                  Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 GPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVSV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
BY SIMILARITY.

BY SIMILARITY.

F6D67D0BB235EA35 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1417;
                                                                                                                                                                                                                                                                        Query Match
10.4%; Score 283.5; DB 1;
Best Local Similarity 24.8%; Pred. No. 3.1e-12;
Matches 131; Conservative 62; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713 AA
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NCBI_TaxID=1410;
                                                                01-NOV-1988
                                 CDGT_BACS0
P05618;
                                                                                                                                                                                                                                                                                                                                                                                                                                     resolution
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 RESULT 13
CDGT_BACS0
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWQKSFWAAVNNY--KPVFTFGEWFLGVNEVGP-ENHKFANESGMSLLDFRFAQKVRQVF 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 GGDWQGIINKIND--GYLTGMGVTAIWISQPVENIYSIINYSGVNNTAYHGYWARDFKKT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRSNRNQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-----PAYGTIADFQNLIAAAHAKNIKVIIDFAPNHTSPA-SSDQPSFAENGRLYDNG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 EVDIENGNYDYLMYADIDMDHPEVINE-----LRNWGVWYTNTLNLDGFRIDAVKHIKY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ENGIYKNL-YDLADLNHNNSTSDVYLKDAIKMW-----LDLGIDGIRMDAVKHMPF 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SNSGGYFDMRNILNGSVVQKHPI-HAVTFVDNHDSQPGEALESFVQSWFKPLAYALILT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQGYPSVFYG--DYYGIPTH-----GVPSMKS------KIDPLLQARQTYAYGTQH 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYFDHHDIIGWTREGDSS------HPN----SGLATIMSDGPGGNKWMYVGKHKAGO 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNHW----NRLRDDAANLKSKGITAVWIPPAWKG-----TSQNDVGYGAYDLYDLGEF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 SYTRDWLTHVRNTTGKPMFAVAEFW--KNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 EISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGKAWDW
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                     Pfam; PF01833; T1G; 1.
ProDom; PD001568; CBD_4; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Calcium; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 TLLGGYTNDTQNLF-------HHNGGTDFSTT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 281; DB 1; Length 713;
; Pred. No. 6.1e-12;
81; Mismatches 189; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                    RAW-STARCH-DIGESTING AMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85FB616DA687B888 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              483 -YNDVLGGLLNGNTLTVGSGGAASNFTLAAGGTAVW 517
                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY
                                                                                                                                                                                                    PIR; A34648; A34648.
PIR; S09196; S09196.
HSSP; P43379; 1CXF.
InterPro; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
InterPro; IPR002909; IPT_TIG.
                                                                                                                                                                                                                                                                                                                                                                                                                   BY
BY
BY
                                                                                                                                                                                                                                                                                                      Pfam; PF00128; alpha-amylase;
Pfam; PF00686; CBD_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X.
                                                                                                                                                                         EMBL; M33302; AAA22239.1; -. EMBL; D90112; BAA14140.1; -.
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260
355
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Matches 116;
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                                                                                                                                                                                                              MEDLINE-87308036; PubMed-2957361; Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.; Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.; "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene of alkalophilic Bacillus sp. strain 1011 and similarity of its amino acid sequence to those of alpha-amylases."; J. Bacteriol. 169:4399-4402(1987).
                                                                                                                                                                                                                                                                                                                                       Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K., "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: MONOMER.
-!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERAINAL SIDE CLEAVES THE ALHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATÁLYTIC ÁCTIVITY: DEGRADE STRCH TO CYCLODEXTRINS BY FORMATION OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
                                                                                                                                                                                                                                                                                                                                                                        Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A resolution.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYCLOMALTODEXTRIN GLUCANOTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001568; CBD_4; 1.
Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
                                             01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
                                                                                                                     Bacillus sp. (strain 1011).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
SIMILARITY.
SIMILARITY.
SIMILARITY.
 713 AA
                                                                                          (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE)
                                                                                                                                                                                                                                                                                                                                                                                                      Acta Crystallogr. D 52:1136-1145(1996)
                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, A26678; ALBSG1.
PDB: 1PAM: 11-JAN-97.
InterPro: IPR000461; Alpha_amylase.
InterPro: IPR002044; CBD_4.
InterPro: IPR00299; IPT_IIG.
Pfam: PF00183; Alpha-amylase; 1.
Pfam: PF01833; TIG: 1.
 PRT;
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STANDARD;
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165
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SEQUENCE FROM N.A., AND SEQUENCE OF 28-44.
MEDLINE=89036108; PubMed=2972812;
Kaneko T., Hamamoto T., Horikoshi K.;
"Molecular cloning and nucleotide sequence of the cyclomaltodextrin glucanotransferase gene from the alkalophilic Bacillus sp. strain no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-586 FROM N.A. Horikoshi K.; Ameko T., Horikoshi K.; Amenoto T., Kaneko T., Horikoshi K.; Amelootide sequence of the cyclomaltrodextrin glucanotransferase (GTRSes) gene from alkalophilic Bacillus sp. strain No. 38-2."; Agric. Biol. Chem. 51:2019-2022(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                   IIGWTREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQV------WRDITGN--RSG 460
                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                        MATINIY -- KPVFTFGEWFLGVNEISPEYHQFANESGMSLLDFRFAQKARQVFRDNIDNM 327
                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                    ::::|||| :: |||:||||| : |||||||||| || XGLKAMLEGSEVDYAQVNDQVTFIDNHDMERFHTSNGDRRKLEQALAFTL---TSRGVPA 384
                                                                                                                                                                                                                                                                                                                                                                                    ----KIDPLLQARQTYAYGTQHDYFDHHD 409
                                                                                                                                                                                                                                                                                                                                                                                                          385 IYYGSEQYMSGGNDPDNRARLPSFSTTTTAYQVIQKLAPLRKSNPAIAYGSTHERWINND 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIIYERKFGN----NVAVVAI------NRNMNTPASITGLVTSLRRASYNDVLGGILNGN 494
                                                                                                                                     70 NQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRSNRNQ 129
                                                                                                                                                           N-----PAYGTWQDFKNLIDTAHAHNIKVIIDFAPNHTSPASSDD-PSFAENGRLYDNG 188
                                                                                                                                                                                                              224
                                                                                                           78 GGDWQGIINKIND--GYLTGMGITAIWISQPVENIYSVINYSGVNNTAYHGYWARDFKKT 135
                                                              Gaps
                                                                                     21 GNHW----NRLRDDAANLKSKGITAVWIPPAWKG-----TSQNDVGYGAYDLYDLGEF
                                                                                                                                                                                    130 EISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGKAWDW
                                                                                                                                                                                                                                      190 EVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYTRDW
                                                                                                                                                                                                                                                   225 -ADLNHNN-----SSVDVYLKDAIK------MIL--DLGVDGIRVDAVKHMPFGWQKSF
                                                                                                                                                                                                                                                                                      LTHVRNTTGKPMFAVAEFW--KNDLA-AIENYLNKTSWNHSVFDVPLHYNLYNASNSGGY
                                                                                                                                                                                                                                                                                                                                     307 FDMRNILNGSVVQKHPIH-AVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPS
                                                                                                                                                                                                              -----HHYGGTDFS---TIENGIYK-----NLYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC 2.4.1.19)
                                        Length 713;
   524B259526B56C52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus sp. (strain 38-2).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_maxID=1412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-1989 (Rel. 10, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
01-WOV-1995 (Rel. 32, Last annotation update)
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR
                                     10.2%; Score 277; DB 1; 22.1%; Pred. No. 1.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE)
                                                                 87; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gen. Microbiol. 134:97-105(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVTINADG-WGNFTVNGGAVSVW 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTVGAGGAASNFTLAPGGTAVW 517
      78340 MW;
                                                                                                                                                                                                                                                                                                                                                                                         VFYGDYYGIPTHGVPSMKS----
                                           Query Match 10.2%
Best Local Similarity 22.1%
Matches 111; Conservative
                                                                                                                                                                                                                  189 NELGGYTNDTQNLF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
       AA;
      713
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       SEQUENCE
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CDGT_BACS3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRSNRNQEIS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGKAWDWEVD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 IENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYTRDWLTH 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.

COCRACTOR: BINDS TWO CALCIUM IONS.

SUBUNIT: MONOMER.

MISCELLANEOUS: GGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
MISCELLANEOUS: GGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GNHW----NRLRDDAANLKSKGITAVWIPP----AWKGTSQNDVGYGAYDLYDLGEFNQK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRNTTGKPMFAVAEFW--KNDLA-AIENYLNKTSWNHSVFDVPLHYNLYNA--SNSGGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INNY -- KPVFNFGEWFLGVNEISPEYHQFANESGM--SLLDFPFAQKARQVFRDNTDNMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYCLOMALTODEXTRIN GLUCANOTRANSFERASE. A1.
B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 275; DB 1; Length 712;
Pred. No. 1.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPGGI -> SWRHL (IN REF. 2).
4FAA8F70BEF818F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD001568; CBD_4; 1.
Transferase; Glycosyltransferase; Calcium; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 22.48; Pred. No. 1.6e
Matches 114; Conservative 90; Mismatches
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PIR; S24193; ALBSG3.
HSSP; P05618; 1PAM.
Interpro; IPR000461; Alpha_amylase.
Interpro; IPR002044; CBD_4.
Interpro; IPR002999; IPP_TIG.
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CC.
DD.
EE.
BBY S
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Pfam; PF00686; CBD_4; 1.
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229
433
522
608
712
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582
712 AA;
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Hofmann B.E., Bender H., Schulz G.E.; "Three-dimensional structure of cyclodextrin glycosyltransferase from Bacillus circulans at 3.4-A resolution.";
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                                                         FYG-DYY------GIPTHGVPS----MKSKIDPLLQARQTYAYGTQHDYFDHHDI 410
                                                                                  386 YYGSEQYMSGGNDPDNRARIPSFSTTTTAYQVIQKLAPLRKSNPAIAYGSTQERWINNDV 445
                                                                                                                                     411 IGWTRE------GDSSHPNS--GLATIMSDGPGGNKWMYVGKHKAGQVWRDITGN 457
                                                                                                                                                                                ...-r YNDVLGG 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nitschke L., Heeger K., Bender H., Schulz G.E.;
"Molecular cloning, nucleotide sequence and expression in Escherichia coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus circulans strain no. 8."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98226626; PubMed-9558324; Schulz G.E.; Schmidt A.K., Cottaz S., Driguez H., Schulz G.E.; Schmidt A.K., Cottaz S., Driguez H., Schulz G.E.; Structure of cyclodextrin glycosyltransferase complexed with a derivative of its main product beta-cyclodextrin."; Blochemistry 37:5909-5915(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein C., Schulz G.E.; "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
11-DEC-1998 (Rel. 37, Last annotation update)
CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appl. Microbiol. Biotechnol. 33:542-546(1990).
[2]
                                                                                                                                                                                446 IIYERKFGNNVAVVAINRNMNTPASITGLVTSLPQGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
                                                                                                                                                                                                                                                                                                                                                             718 AA.
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                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus circulans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           CDGT_BACCI
P30920;
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SUBUNIT: MONOMER.

MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE MALTOOLIGOSACCHARIDE PRODUCED.

SIMILARIY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Glycosyltransferase; Calcium; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000461; Alpha_amylase.
InterPro; IPR002044; CBD_4.
InterPro; IPR002909; IPT_IIG.
DFam; PF00128; Alpha-amylase; 1.
Pfam; PF00686; CBD_4; 1.
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B.
C.
D.
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BY
BY
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84
258
291
362
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8CGT; 14-OCT-98.
9CGT; 14-OCT-98.
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27-MAY-98.
12-AUG-98.
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14-OCT-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01833; TIG;
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477
51
73
73
73
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83
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408 HD-------IIGWTRECDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDI 454 : | : | : | : | : | : | 450 NDVYVYERKFGKSVAVVAVNRNLSTSASITGLSTSLPTGS------YTDV 493 193 IENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYTRDWLTH 252 253 VRNTIGKPMFAVAEFWKNDLAA---IENYLNKTSWNHSVFDVPLHYNLYNA--SNSGGYF 307 280 I--YAHKPVFTFGEWFLGSAASDADNTDFANKSGM--SLLDFRFNSAVRNVFRDNTSNMY 335 308 DMRNILNGSVVQKHPIH-AVTFVDNHDSQPGEALESFVQSWF--KPLAYALILT-REQGY 363 336 ALDSMINSTATDYNQVNFFIDNHD-----MDRFKTSAVNNRRLEQALAFTLTSRGV 389 364 PSVFYGDYYGIPTHGVPSMK------SKIDPLLQARQTYAYGTQHDYFDH 407 73 GTVRTKYGTRSQLQGAVTSLKNNGLQVYGDVVMNHKGGADGTEMVNAVEVNRSNRNQEIS 132 142 --INPYFGIMADFQNLITTAHAKGIKIVIDFAPNHTSPAMETD-TSFAENGRLYDNGTLV 198 133 GEYTIEAWTKEDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGKAWDWBVD 192 Gaps 21 GNHW----NRLRDDAANLKSKGITAVWIPP----AWKGTSQNDVGYGAYDLYDLGEFNQK 72 199 GGYT-----NDTNGYF----HNGGSDFS---SLENGIXK-----NLYDL-AD Indels 119; DB 1; Length 718; Query Match
10.1%; Score 274.5; DB 1;
Best Local Similarity 22.2%; Pred. No. 1.7e-11;
Matches 113; Conservative 87; Mismatches 191; 455 TGN--RSGTVTINADGWGNFTVNGGAVSVW 482 QQ ΟŊ Dp Qγ qq QY ρp Ω ΩD ΟÝ QΥ QΥ qq QΥ Dp

Search completed: November 28, 2001, 17:03:58 Job time: 321 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

November 28, 2001, 16:59:02; Search time 21.38 Seconds

(without alignments)
1728.001 Million cell updates/sec

Title:
Perfect score: 2713
Sequence: 1 HHNGTNGTMMQYFEWHLPND......ADGWGNFTVNGGAVSVWVKQ 485
Scoring table: BLOSUMG.2
Gapop 10.0, Gapext 0.5
Searched: 219241 seqs, 76174552 residues
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
2: pir2:*
3: pir2:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	alpha-amylase (EC alpha-amylase (EC alpha-amylase (EC		alpha-amylase (EC alpha-amylase (imp alpha-amylase (EC alpha-amylase (EC cytoplasmic alpha-	alpha-amylase (EC beta-amylase (EC 3 alpha-amylase (EC alpha-amylase (EC alpha-amylase (EC	alpha-amyldse (EC probable alpha-amy glucan 1,4-alpha-m cyclomaltodextrin alpha-amylase (EC cyclomaltodextrin glucan 1,4-alpha-m cyclomaltodextrin	cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin cyclomaltodextrin
SUMMARIES	A27705 A54541 ALBSL	A24436 A24436 ALBSN ALBSF	S15713 C86781 B45738 A45738 B85810	A19506 A29130 S31478 S14958 S10514	109942 205672 20567 509196 705521 AALBSG1 A32803	ALBSGC ALBSGC ALBSG7 ALBSG6
DB			22442		70000101	11211
Length	518 549 512	5149	4 9 9 3 4 9 9 3 4 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9 5 9	217 1196 482 440 421	428 713 713 713 713 712	718 713 713 718
% Query Match	88.8 70.4 70.3	67.9	49.6 41.8 38.8 37.7	14.5 11.6 11.6 10.8	010000000000000000000000000000000000000	10.1 10.0 10.0 9.9
Score	2410 1910.5 1906	1894.5 1843 1833	1347 1133 1053 1022 1006	393.5 315 304.5 294 287.5	286.5 283.5 281 281 277 277 275	274.5 271 270 270 269.5
Result	- 200	* 10 10 10 10	10 11 12	13 14 17 17	2 2 2 2 2 3 2 3 2 3 2 3 2 3 2 3 2 3 2 3	26 27 28 29

241 IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300

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$\begin{array}{c} \omega \omega \omega \omega \omega \omega \omega \omega \omega \omega $	SULT 1 7705 Pha-amylase (EC 3.2.1.1) precursor - Bacillus Aba-amylase (EC 3.2.1.1) precursor - Bacillus Species: Bacillus sp. Date: 31-Mar-1989 #sequence_revision 18-Aug-19 Accession: A27705 Fuckamoto, A.; Kimura, K.; Ishii, Y.; Takano, ochem. Blophys. Res. Commun. 151, 25.31, 1988 reference number: A27705; MUD: 88162814 Accession: A27705 Accession: A27706 Accession: A2	NGTMMQYE INTINII NGTMMQYE NGTMMQYE LGEFNQKC LIIIIII LGEFNQKC LIIIIIII NRNQEISC NRNQEYTC
266.5 266.5 266.5 267.5 267.5 260.5 260.5 260.5 257.5 257.5 257.5 257.5	RESULT 1 A27705 alpha-amylase (EC 3.2 alpha-amylase (EC 3.2 Species: Bacillus s C; Dete: 31-Mar-1989 C; Accession: A7705 R; Tsukamoto, A.; Kimu Bloocham. Bloophys. Res A; Accession: A7705 A; Accession: A770)
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Alba-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis manes: 1.4-alpha-D-glucan glucanohydrolase assession and the anaes: 1.4-alpha-D-glucan glucanohydrolase assession and the anaes: 1.4-alpha-D-glucan glucanohydrolase assession and the anaes and the anaes: 1.4-alpha-b-glucanohydrolase assession assession and the anaes and anaes anaes and anaes and anaes anaes and anaes anaes and anaes an
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                                                                                                   VFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSSHPNSG 425
                                 306 YFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPS
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: chromosomal DNA of strain DN1792
C; Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: 1,4-alpha-D-glucan glucanohydrolase (strain DN1792)
N; Alternate names: 1,4-alpha-D-glucan glucanohydrolase (species: Bacillus stearothermophilus c; Species: Bacillus stearothermophilus C; Date: 28-oct-1994 #sequence_revision 18-aug-1995 #text_change 13-Jun-1997 C; Accession: A54541
R; Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B. FEMS Microbiol. Lett. 77, 271-276, 1991
A; Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus. A; Reference number: A54541
A; McCossion: A54541
A; McCossion: A54541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSY 245
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                                                                                                                                         QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS 420
                                                                                                                                                                Gaps
IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENYLQKTNWNHSVFDVPLHYNLYNA 333
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68.8%;
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A;Cross-references: GB:X59476
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C;Function:
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Matches 329;
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for plasmid

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A 2439
A plan-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
A plan-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus
C Species: Bacillus Stearothermophilus
A Steepence number: A 91817; WIU: 86195857
A Fittle: Structural genes encoding the thermophilus alpha-amylases of Bacillus stearo
A Freedence number: A 91817; WIU: 86195857
A Reference number: A 91817; WIU: 86195857
A Reference number: Back of Strain NZ-3
A Reference number: Back of Strain NZ-3
A Reference number: I Sono; C Species of Strain NZ-3
A Reference number: I Sono; O Strain NZ-3
A Residues: Series preliminary: translated from GB/EWBL/DBJ
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Gaps
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68.6%; Pred. No. 1.2e
iive 70; Mismatches
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Matches 328; Conservative
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IYVQR 512
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                                                                                                                                                         A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 30-37, E', 39-41, X', 43-47 < KUH>
R; Machius; M; Misdand, G; Huber, R.
J; Mol. Biol. 246, 545-559, 1995
A; Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha
A; Reference number: S53788; MUID:95182462
A; Residues: S3788; MUID:95182462
A; Residues: D', 220-227 < MAC>
A; Residues: D', 220-227 < MAC>
A; Residues: M; Wiegand, G; Huber, R.
Bubmitted to the Brookhaven Protein Data Bank, July 1995
A; Reference number: A65206; PDB:1BPL
A; Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-3, A; Note: these structural studies suggest 163 is Leu rather than Arg
R; Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
submitted to the Brookhaven Protein Data Bank, October 1996
A; Reference number: A6680; PDB:1VJS
A; Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-3, A; Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-3, A; Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-3, A; Contents: annotation; X-ray crystallography, 1.7 angstroms.
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            A;Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499 R;Kuhn, H; Fietzek, P.P.; Lampen, J.O. Bacteriol. 1459, 372-373, 1982 A;Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-aA;Reference number: A26151; MUID:82098050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 TRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGG
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69.1%; Pred. No. 4.5e-122;
tive 67; Mismatches 73;
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Matches 335; Conservative
                                                                                                                                            A; Accession: A26151
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A, Accession: A92389
A, Moceale type: DNA
A, Moceale type: DNA
A, Moceasion: A93389
A, Moceale type: DNA
A, Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA
A, Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA
B; Chung, H.S.; Friedberg, F.
B; Chung, H.S.; Friedberg, F.
B; Chung, H.S.; Friedberg, F.
A; Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.
A; Reference number: A90307; MUD:80241725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens
Nyliternate names: 1,4-alpha-D-giucan glucanohydrolase
Nyliternate names: 1,4-alpha-D-giucan glucanohydrolase
C;Species: Bacillus amyloliquefaciens
C;Species: Bacillus amyloliquefaciens
C;Date: 30-Nov-1980 Heaquence_revision 30-Jun-1987 *text_change 18-Jun-1999
C;Accession: A92389; A90307; I39756; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced
A;Reference number: A92389; MUD:83108808
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A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Palya, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund,
Gene, 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region
A;Reference number: 139756; MUID:82051296
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Coss_references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
A;Cross_references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
B;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, SGene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase
A;Reference number: I39763; MUID:88137952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGK
                                 246 TRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGG
                                                                                                                                        AWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSY
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A; Residues: 1-39 <RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
B;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didertchsen, B.
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didertchsen, B.
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid of A;Reference number: 139772; MUID:91092499
A;Accession: 139772; MUID:91092499
A;Accession: 139772; MUID:91092499
A;Accession: 139772; MUID:91092499
A;Accession: 145 ARS
A;Residues: 1-45 ARS
A;Cross-references: GB:M62638; NID:9142514; PIDN:AAA22242.1; PID:9142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the source of the sou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Reywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; pc
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;35-549/Domain: alpha-amylase core homology <AMY>
F;35-549/Domain: alpha-amylase core homology <AMY>
F;368,237.272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,365/Active site: Asp, Glu, Asp #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5 N, Alternate names: 1,4-alpha-D-glucan glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; 139777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSF
                                                                                                                             306 YFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPS
                                                                                                                                                                                                                                                                                                                                                                     366 VFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSSHPNSG
                                                                                    TRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGG
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Pred. No. 3e-121;
); Mismatches 80;
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J. Bacteriol. 163, 401-406, 1985
A; Reference number: A24436; MUID:85234394
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Matches 327; Conserv
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A; Residues: 1-549 <NAK>
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Residues: 1-29,'Q',31-75,'W',77-122 <TSU>
Comment: Alpha-amylase genes have been found on plasmids and in multiple copies
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A;Mostdues: 35.48 < IHZ.
A;Essidues: 35.48 < IHZ.
A;Experimental source: strain DY-5
R;Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata, D. Bacteriol. 164, 1182-1187, 1395
A;Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
A;Reference number: A91804; MUID:86059211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DY-5) plasmid
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NyAlternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Species: Bacillus stearothermophilus
C;Date: 30-dun-1887 **sequence_revision 30-Jun-1987 **text_change 16-Feb-1997
C;Accession: A91999; B91999; A91804; A00845
R;Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Udaka, S.
J. Blochem. 98, 95-103, 1985
A;Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase gene: homology of the complete nucleotide sequence of a thermophilic alpha-amylase and the complete nucleotide sequence of a thermophilic alpha-amyla
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                                                                                                                                                                                                                                                                                           SAVNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYD 89
                           F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted F;262,292,359/Active site: Asp, Glu, Asp #status predicted
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                                                                                                                                       Length 514;
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A; Residues: 1-548 <IH1>
A; Residues: 68: X02769
A; Cross-references: GB: X02769
A; Experimental source: plasmid pH1300 from strain DY-5
A; Accession: B91999
                                                                                                                                       67.9%; Score 1843; DB 1;
Similarity 66.4%; Pred. No. 8.6e-118;
24; Conservative 68; Mismatches 88;
   <AMX>
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homology
alpha-amylase core
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A; Molecule type: DNA
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F; 229-362/Domain:
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Best Local Simil
Matches 324; (
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Albania ampliase (EC 3.2.1.1) - Bacillus circulans
C; Specias Bacillus circulans
C; Specias Bacillus circulans
C; Specias Bacillus circulans
C; Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Accession: S15713
R; Marcel, T.
submitted to the EMBL Data Library, May 1991
A; Reference number: S15713
A; Reference number: S15713
A; Reference number: S15713
A; Residues: 1-493 <AAR>
A; Residues: 1-493 <AAR>
A; Residues: 1-493 <AAR>
A; Residues: EMBL: X60779; NID:g39411; PIDN: CAA43194.1; PID:g39412
C; Genetics:
A; Gene: amyE
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A; Pathway: g1ycogen/starch degradation
C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
                                                                                                                                                                                                                                                                        polys
                                                                                                                                                                                                                                          core homology
                                                                                                                                                                              of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                       type; alpha-amylase core homolog
heat-stable protein; hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 NRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGAYDLYD 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 NGTWMQYFEWYLPDDGTLWTKVANEANNLSSLGITALSLPPAYKGTSRSDVGYGVYDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 TRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 YFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 AWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSY
                                                                                                                                                                                                                                                                                                                                                                                    predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
A; Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
C; Comment: Alpha-amylase genes have been found on plasmids and 1
C; Genetics:
A; Genome: plasmid
A; Start codon: GTG
C; Function:
A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-A; Pathway: glycogen/starch degradation
C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amyl C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amyl c; Keywords: extracellular protein; glycosidase; heat-stable prot F; 1-34/Domain: signal sequence #status predicted <SIG>F; S5-548/Product: alpha-amylase fstatus experimental <NAT>F; 235-368/Domain: alpha-amylase core homology <AMY>F; 139, 237, 272, Binding site: calcium (ABP, ASP, His) #status predicted
F; 268, 298, 365/Active site: ASP, Glu, ASP #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1833; DB 1;
Pred. No. 4.5e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.6%; Sco. 66.9%; Pred. No. ...
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A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Deskription: catalyzes the hydrolysis of internal 1,4-alpha-amylase core homology C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C; Reywords: cytosol; glycosidase; hydrolase; polysaccharide degradation F; 202-335/Domain: alpha-amylase core homology <AMY> F; 239, 265, 332/Active site: His, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGKAMDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRG-- 182
                                                                                                                                                                                                                                                                                                                                                  FDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPSV 366
                                                                                                                                                                                                                                                                                                                               367 FYGDYYGIPTHGYPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSSHPNSGL 426
                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-494 <RAH>
A; Cross-references: GB:LO1643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 NGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQN-DVGYGAYDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILTINKNGGSKYMIIDKAYAGKVYIDLFGRHEIPITLDQNGGAEFYVNDGSVSVWV 476
                                                                                                                                                                                                                                                                                                                                                                                               ATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVSVWV 483
                                                                                                                                                                                                                                                                                  247 RDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGGY
                                                                 RNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGKA
                                                                                       WDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYT
GEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.8%; Score 1053; DB 1;
ilarity 42.1%; Pred. No. 3.8e-64;
Conservative 84; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 207; Conserva
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C;Species Lactococcus lactis subsp. lactis
C;Species Lactococcus lactis subsp. lactis
C;Species Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86781
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
A;Accession: C86781
A;Accession: C86781
A;Status: preliminary
A;Molecule type: DNA
A;Gratus: preliminary
A;Molecule type: DNA
A;Grast-references: GB:ABO05176; NID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146
A;Experimental source: strain IL1403
A;Gractics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: amyL
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 VFYGDYYGIGGPEPVDG---KKEILDILLISARCNKAYGEQEDYFDHANTIGWVRRGVEEI 419
                                                                                                                                                                                                                                                                                                                                                                                                                        243 IKEFAAEMIRKRGQDFYIVGEFWNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLKGR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 YEDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQGYPS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFYGDYYGI----PTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSSH 421
                                                                                                                                                                                                                                                                    NRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRGTGK 185
                                                                                                                                                                                                                                                                                       305
                                                                                                                                                                                                                     66 LGEFNOKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRS 125
                                                                                                                                                         6 NGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGAYDLYD 65
                                                                                                       Gaps
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                                                                         Length 493;
     degradation
                                                                                                         Indels
                                                                       Match.
Local Similarity 51.4%; Pred. No. 4e-84;
les 247; Conservative 73; Mismatches 153;
        C; Keywords: glycosidase; hydrolase; polysaccharide F; 200-333/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Si
Matches 205;
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D.J.; May
K.; Apoda
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <STO>
A;Cross-references: GB:AE005174; NID:q12516028; PIDN:AAG56942.1; GSPDB:GN00145; UMGP:
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Gene: amyA
:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
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                                                                 181
                                                                                                                                                                                    243 YSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASN 302
                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                412
                                                                                                                                                                                                                                                                                                                                                                         362 VPSVFYPDLYGAHYEDVGGDGQTYPIDMPIIEQLDELILARQRFAHGVQTLFFDHPNCIA 421
                                                                                                                                                                                                                                                                                                                                                                                                                             472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKFRG-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 YSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             413 WTREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQN-DVGYGAYDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NPTLLQCFHWYYPEGGKLWPELAERADGFNDIGINMVWLPPAYKGASGGYSVGYDSYDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGKAWDWEVD1ENGNYDYLMYAD1DMDHPEV1NELRNWGVWYTNTLNLDGFR1DAVKH1K
                                                                                                         TGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 TVNGGAVSVWV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 200;
                                                                                                                                          182
                                                                                                                                                                                                                                                                  303
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A; Residues: 1-495 cMLAT>
A; Cross-references: GB:AE000285; GB:U00096; NID:g1788229; PIDN:AAC74994.1; PID:g1788236; A; Cross-references: GB:AE000285; GB:U00096; NID:g1788229; PIDN:AAC74994.1; PID:g1788236; B; Raha, M.; Kawaqishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A; Bacteriol. Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A; Reference number: A45738; MUID:93015717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amylase (EC 3.2.1.1), cytosolic - Escherichia coli
NyAlternate names: 1,4-alpha-D-glucan glucanohydrolase
(Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 07-Apr-1994 #sequence_revision 31-0ct-1997 #text_change 18-Jun-1999
C;Accession: D64956; A45738
R;Blattner, F.R; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V; Riley, 1.A.; Rose, D.J.; Mau, B.; Shao, Y.
A; Rose, D.J.; Mau, B.; Shao, Y.
A; Reference number: A64720; MUID:97426617
A;Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloliquefaciens type: alpha-amylase core homology
C:Superfamily: alpha-amylase, phydrolase; polysaccharide degradation
F:202-335/Domain: alpha-amylase core homology <AMY>
F:104,204,239/Binding site: calcium (Asn, Asn, His) #status predicted
F:235,265,332/Active site: Asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 DLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAVEVNR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-18, SS',21-108,'V',110-148,'E',150-233,'I',235-495 <RAH>
A;Cross-references: GB:L01642; NID:g146021; PIDN:AAA23810.1; PID:g146023
C;Genetics:
242 AWFYKEWIEHVQAVAPKPLFIVAEYWSHEVDKLQIYIDQVDGKIMLFDAPLQMKFHEASR
                                                                                                                                                                 362 VPSVFYPDLYGASYEDSGENGETCRVDMPVI-NQLDRLILARQRFAHGIQTLFFDHPNCI
                                                                                                                                                                                                                                                                                                      412 GWTREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGN
                                                                                                                                                                                                                                                                                                                                 YSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASN
                                                                                                                                                                                                                      363 YPSVFYGDYYGIPTH------GVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDII
                                                                                                                                          SGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.7%; Score 1022; DB 1; 41.1%; Pred. No. 4.8e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.77
Best Local Similarity 41.15
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        FFCNAGSVSVWV 490
                                                                                                                                                                                                                                                                                                                                                                                     472 FTVNGGAVSVWV 483
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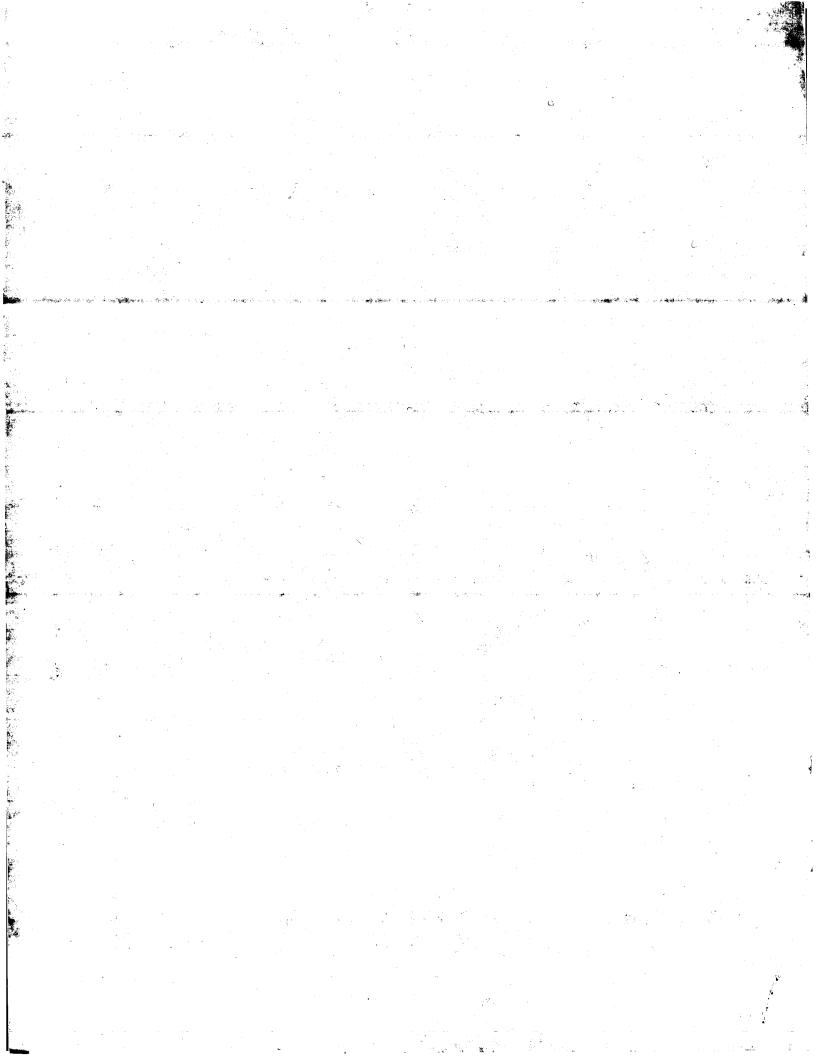
5,

N.; Ud

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of internal 1,4-alpha-D-glucosidic bonds activity)
    Deta-amylase (EC 3.2.1.2) / alpha-amylase (EC 3.2.1.1) precursor - Bacillus polymyxa C; Species: Bacillus polymyxa Dolymyxa C; Date: 25-Oct-1987 #sequence_revision 03-Mar-1994 #text_change 15-Oct-1999 C; Accession: A29130; B29130; A32251; A29108 R; Kawazu, T.; Makanishi, Y.; Uozumi, N.; Sasaki, T.; Yamagata, H.; Tsukagoshi, N.; Ud J. Bacteriol. 169, 1564-1570, 1987 A; Title: Cloning and nucleotide sequence of the gene coding for enzymatically active A; Reference number: A29130; MUID:87165765 A; Molocular A29130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A29108
A; Molecule type: DNA
A; Residues: MIGL', 2-66, 'S', 68-99, 'D', 101-153, 'N', 155-176, 'Q', 178-226, 'KS', 229-329,'
A; Experimental source: ATCC 8523
                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 3f-50 (*A.S.).
A; Residues: 3f-50 (*A.S.).
B; Uozumi, N.; Sakural, K.; Sasaki, T.; Takekawa, S.; Yamagata, H.; Tsukagoshi,
J. Bacteriol. 171, 375-382, 1989
A; Title: A single gene directs synthesis of a precursor protein with beta- and
A; Reference number: A32251; MUID:89123046
A; Accession: A32251
A; Status; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDV-GYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYGGFNSNNSDQRKWH----GGDFQGIINKLDYIKNMGFTAIWITPVTMQKSEYAYHGYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVKHIKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 VEVNRSNRNQEISGEYTIEAWTKFDF-PGRGNTHSNF-KWRWYHFDG--TDWDQSRQLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIYKFRGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymyxa beta amylase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A) Description: catalyzes both the hydrolysis of internal 1,4-alp vely from the non-reducing end (beta-amylase activity)
A) Pathway: glycogen/starch degradation
C; Superfamily: alpha-amylase core homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 1-35/Domain: signal sequence #status predicted <SIG>F; 36-1196/Peroduct: beta-amylase/alpha-amylase #status predicted
F; 908-1033/Domain: alpha-amylase core homology <AMY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score 315; DB 2;
ilarity 24.1%; Pred. No. 1.6e-13;
Conservative 67; Mismatches 189;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. Experimental source: strain 72
R;Rhodes, C.; Strasser, J.; Friedberg, F.
Nucleac Acids Res. 15, 3934, 1987
A;Title: Sequence of an active fragment of A;Reference number: A29108; MUID:87231094
                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-936 <KAM>
A,Cross-references: GB:M15817
A,Experimental source: strain 72
A,Accession: B29130
A,Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 937-1196 <UOZ>
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Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-56;57-144 <SAC>
A; Residues: 1-56;57-144 <SAC>
A; Note: residues: 1-56;57-144 <SAC>
B; Note: residues: 1-56;57-140 <BC 
R; Detera, S.D.; Friedberg, F.
Int. J. Pept. Protein Res. 17, 93-106, 1981
A; Title: Sequence of the CNBr peptide containing the putative essential tyrosine of Baci A; Reference number: A91759; MUID:81191186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A; Pathway; glycogen/starch degradation C; Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology C; Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: this sequence corresponds to residues 398-469 of the complete sequence Comment: See PIR:ALBSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Bacillus amyloliquefaciens
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C;Accession: A91760; A91759; A19506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKAVEFVENTESLPGH-----FKPLSVDTGRLPNDVEALSQDGFTLQETHQFKAYW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGGYFDMRNILNGSVVQKHP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 YADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYTRDWLTHVRNTTGKPMF 262
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                 363 YPSVFYGDYYGIPTHGVPS------MKSKIDPLLQARQTYAYGTQHDYFDHHDIIG 412
                                                                                                                                                                                WTREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNF 472
242 AWFYKEWIEHVQEVAPKPLFIVAEYWSHEVDKLOTYIDQVEGKTMLFDAPLQMKFHEASR
                                                             SGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTREQG
                                                                                         :66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-amylase (EC 3.2.1.1) - Bacillus amyloliquefaciens (fragments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 393.5; DB Pred. No. 8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDHHDIIGWTREGDSSHPNSGLATIMSDGPGGNK 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Sachdev, O.; Friedberg, F.
Int. J. Pept. Protein Res. 18, 228-236, 1981
A;Reference number: A91760; MUID:82189140
A;Accession: A91760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 IHAVTFVDNHDSQPGEALESFVQSWFKPLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%;
34.3%;
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Residues: 145-217 <DET>
                                                                                                                                                                                                                                                                                                                                      473 TVNGGAVSVWV 483
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Matches
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1	Db 408 WVDDTFYAFQRSYNGDEVVVMINNSWNSQTRTVPNIDRVANGQTLYNRMGTDKVTVNNGS Qy 479 VS 480	Db 468 IT 469	Search completed: November 28, 2001, 16:59:03 Job time: 196 sec		6	Heese, O.; Hansen, G.; H amylase from Thermoactin		bonds	24;								
	QY 296 NLYNASNSGSYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESF 343	QY 344 VQSWFKPLAYALILT-REQGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQH 402	QY 403 DYFDHHDIIGMTREGDSSHPNSGLATIMSDGPGGNKWMYVGKHKAGQ 449 1	QY 450 VWRDITGNRSGTVTINADGWGNFTVNGGAVSV 481 	RESULT 15 S31478 alpha-amylase (EC 3.2.1.1) - Thermoactinomyces vulgaris C;Species: Thermoactinomyces vulgaris C;bate: 22-Nov-1999 #sequence_revision 10-Nov-1995 #text_change 22-Oct-1999	C., Accession: 3314.78 R. Hofemeister, B. F. Koenig, S.; Hoang, V.; Engel, J.; Mayer, G.; Heese, O.; submitted to the EMBL Data Library, December 1992 A.; Description: The gene amyTV coding for a non-glucogenic alpha-amylase from the R. Reference number: \$31478 A.; Accession: \$31478 A.; Molecule type: DNA	A. Residues: 1-482 <hof> A. Gross references: EMBL:X69807; NID:g48289; PIDN:CAA49465.1; PID:g48290 C. Function:</hof>	A:Description: catalyzes the hydrolysis of internal 1.4-alpha-D-glucosidic bonds A:Pathway: glycogen/starch degradation C;Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology C;Keywords: glycosidase; hydrolase; polysaccharide degradation F:194-319/Domain: alpha-amylase core homology <amy></amy>	Query Match Best Local Similarity 24.1%; Pred. No. 2.5e-13; Matches 116; Conservative 62; Mismatches 171; Indels 133; Gaps	QY 34 LKSKGITAVWIPPAWKGTSONDV-GYGAYDLYDLGEFNQKGTVRTKYGTRSOLOGAVTSL 92 : : :	QY 93 KNNGIQVYGDVVMNHKGGADGTEMVNAVEVNRSNRNQEISGEYTIEAWTKFDFPGRGNTH 152 1 1 1 1 1 1 1 1 1	QY 153 SNFKWRWYHPDGTDWDQSRQLQNKIYKFRGTGKAWDWEVDIENGNYDYLMYADIDMDH 210	Qy 211 PEVINELRNWGVWYTNTLNLDGFRIDAVKHIKYSYTRDWLTHVRNFTGKDWFAVAEFWKN 270	OY 271 DLAAIENYLNKTSWNHSVFDVPLHYNLYNASNSGYFDMRNILNGSVVQKHPIHAVT 327 1	Qy 328 FVDNHDSQPGBALESFVQSWFKPLAVALILTREQGYPSVFYGDYYGIPTHG 378 1:	OY 379 VPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSSHPNSGLATIMSDGFGGNK 438 10	Qy 439 WMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGA 478



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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-720-899-1 + 1909.00 3559.20 /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-610-1 + 1909.00 3559.20 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-343-804-1 + 1909.00 3559.20 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-343-804-1 + 1909.00 3559.20 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-680-908A-1 + 1909.00 3559.20 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-680-908A-1 + 1909.00 3559.20
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hartington, James J.
REGISTRATION NUMBER: 38,711
REPERBENCE/DOCKET NUMBER: 4157.204-US
TELECHONE: (212) 867-0123
TELEPHONE: (212) 878-9555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-446-803-4 from: 1
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US-09-590-375-2 x US-08-446-803-4
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US-08-446-803-4
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STRANDEDNESS: single
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Percent Similarity: 99.381
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(9972_6/ptodata/Z/lina/fa_COMB.seq; 195.0-646 | 191.0 |

(9972_6/ptodata/Z/lina/fa_COMB.seq; 195.0-646 | 191.0 |

(9972_6/ptodata/Z/lina/fa_COMB.seq; 195.0-616 | 191.0 |

(9972_6/ptodata/Z/lina/fa_COMB.s
                                                                                                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
   out_format : pfs
OM of: US-09-590-375-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-09-590-375-2
Query length: 485
Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
Search time (sec): 64.100000
                                                                                                                                                                                                                                        Command line parameters:
                                                                   Date: Nov 28, 2001
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1.3e-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GCCAAATGACGGGAATCATTGGAACAGGTTGAGGGATGACGCAGCTAACT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL
                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRI.

2.PF: 10174

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
FTLING DATE: 01-June-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 95.052
                                                                                                                                                                                   Sequence 4, Application US/08446803
Sequence 4, Application Ottory, Helle
APPLICANT: Disparate Henrik APPLICANT: Rasmussen, Michael Dolberg APPLICANT: Nanussen, Michael Dolberg TILLE OF INVENTION: Alkaline Bacillus Amylase NUMBER OF SEQUENCES: Second Correspondence ADDRESS:
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SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
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TrggaaaatgacCTTGGTGCAATTGAAACTATTGAATAAAACAAGTT
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                                                                                                                        yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
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SSEE: No. 58561640 No. 5856164disk of No. 5856164th America
1: 405 Lexington Avenue
New York
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yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
                                                                                                          erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                                                                                                                                                            TrpArgAsp1leThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ottrup, Helle
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-June-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-June-199 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1451 AGCAA 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                           484 ysGln 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                       Length: 485
Gaps: 0
Identity: 95.052
                                                                                                                                                                                                                 to: 1455
                                                                                                                                                                                                                from: 1
                                                                                                                                                            Percent
                                                                                                                                                                                                                Align seg 1/1 to: US-08-861-837-4
                                                                       TOPOLOGY: linear

HOLECULE TYPE: DNA (genomic)

US-08-861-837-4
                                                                                                                                                                                          US-09-590-375-2 x US-08-861-837-4
(212) 867-0123
          TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                 . Ratio: 5.421
Percent Similarity: 99.381
                                                                                                                                       2613.00
                                                                                                                                        Quality:
TELEPHONE:
                                                                                                                             alignment_scores
                                                                                                                                                                                  alignment_block
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                                                                                                                                                             GGAATCACTCGGTGTTTGATGTTCCTCTCCACTATAATTTGTACAATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
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              rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                                                                                                                                                                                     rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                                                                                                                                                                                                                                                          SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                                                                                                                                                                                                                                                         erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
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                                                                    434 roGlyGlyAsnLysTrpMetTyrValGlyIysHisLysAlaGlyGlnVal
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                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
   Sequence 4, Application US/08600656
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ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
COUREMANE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: 13-FEB-1996
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
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Gaps: 0
Percent Identity: 95.052
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       APPLICANT: Bisgard-Frantzen, Henrik APPLICANT: Svendsen, Allan APPLICANT: Borchert, Torben Vedel TITLE OF INVENTION: AMYLASE VARIANTS NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: US-08-600-656-4
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US-09-590-375-2 x US-08-600-656-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1455 base pairs
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Ratio: 5.421
Percent Similarity: 99.381
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STRANDEDNESS: single
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GENERAL INFORMATION:
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                                                                                                                                                                                                                    SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
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                                                                                                                                                                      uargasnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
     117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                       ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
                            GlyaspvalvalmetasnHisLysGlyGlyalaAspGlyThrGluMetVa
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1401 CGGATGGGGTAATTTCTCTGTTAATGGAGGGTCCGTTTCGGTTTGGGTGA 1450
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                                                                                    417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
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GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
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Percent Identity:
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    Sequence 9, Application US/09170670
    Patent No. 6187576
    GENERAL INFORMATION:
    APPLICANT: Svendsen, Allan
    APPLICANT: Svendsen, Allan
    APPLICANT: Brochert, Torben
    APPLICANT: Brochert, Torben
    TITLE OF INVENTION: Alpha-amylase Mutants
    FITLE REFERENCE: 5276.200-US
    CURRENT APPLICATION NUMBER: US/09/170,670
    CURRENT FILING DATE: 1998-10-13
    EARLIER APPLICATION NUMBER: 66/063,306
    EARLIER PILING DATE: 1997-10-13
    EARLIER PILING DATE: 1997-10-13
    EARLIER PILING DATE: 1997-10-13
    SEALIER PILING DATE: 1997-10-28
    NUMBER OF SEQ ID NOS: 22
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 9
    INMATH. 14.55
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US-09-590-375-2 x US-09-170-670-9
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nilarity: 99.381
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                                                        201 AGAGTTTAACCAGAAGGGGACGGTTCGTACAAAATATGGAACACGCAACC
                                                                                           101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa
                                                                                                                                         117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
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                                  yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
                                                                               84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
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uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL

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                                                                                                            TrpArgAsplleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                                                                                                                       GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
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Gaps: 0
Percent Identity: 95.052
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APPLICANT: Sorchert, Torben
APPLICANT: Bisgard-Frantzen Henrik
APPLICANT: Bisgard-Frantzen Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-05
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT APPLICATION NUMBER: 112/97
EARLIER APPLICATION NUMBER: 60/063,306
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09170670 Patent No. 6187576 GENERAL INFORMATION:
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LENGTH: 1455
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                                                                                                                                               lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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151 ACTICCCAGAAIGAIGIAGGIIAIGGAGCCIAIGAITIAIAIGAICTIGG 200
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                             euLysSerLysGly11eThrAlaValTrpI1eProProAlaTrpLysGly
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US-09-590-375-2 x US-09-193-068-9

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                                                                                                                                                 317 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS
                                                                        334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
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Percent Identity: 95.052
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APPLICANT: SvendSen, Allan
APPLICANT: Bisgaard Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709.000-US
CURRENT APPLICATION NUMBER: US/09/193,068
UURBENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
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. Sequence 9, Application US/09193068:
. Patent No. 6197565
. GENERAL INFORMATION:
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Ratio: 5.421
nilarity: 99.381
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US-09-193-068-9
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                                                                               51 ThrSerGlnasnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl
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                       1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
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to: US-09-193-068-9
Align seg 1/1
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TGGAGAGATATTACCGGAAATAGGACAGGCACCGTCACAATTAATGCAGA 1400
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                                                                        317 lvalGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334
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301 SerAsnSerClyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                   TCTAATAGCGGTGGTTATTATGATATGAGAAATATTTTAAATGGTTCTGT
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APPLICANT: Kjrulff, S ren
APPLICANT: Risgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REPERBENE: 5709,000-02
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID.NOS: 31
SEQ ID.NO 13.0
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CORGANISM: Bacillus
US-09-193-068-13
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ThrHisvalArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
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 Length: 485
Gaps: 0
Identity: 95.052
                                       to:
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                                       Align seg 1/1 to: US-09-193-068-13
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US-09-590-375-2 x US-09-193-068-13
   2613.00
              99.381
         Ratio:
     Quality:
              Percent Similarity:
alignment_scores
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GGTGCAAAAACATCCAACACATGCCGTTACTTTTGTTGATAACCATGATT 1000
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                                                                                                            ACACATGTGCGTAACACCACAGGTAAACCAATGTTTGCAGTGGCTGAGTT
                              eTrpLysAsnAspLeuAlaalaIleGluAsnTyrLeuAsnLysThrSerT
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    Sequence 9, Application US/09183412
    Patent No. 6204323
    GENERAL INFORMATION:
    APPLICANT: Borchert, Torben V.
    APPLICANT: Borchert, Allan
    APPLICANT: Andersen, Carsten
    APPLICANT: Andersen, Carsten
    APPLICANT: Nielsen, Bjarne
    APPLICANT: Niesen, Torben L.
    APPLICANT: Nissen, Torben L.
    APPLICANT: Riaerulff, Soren
    TITLE OF INVENTION: Alpha-Amulase Mutants
    FILE REFERENCE: 5368 200-US
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184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 AGAGTTTAACCAGAAGGGGACGGTTCGTACAAAATATGGAACACGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
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Gaps: 0
Percent Identity: 95.052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1455
           EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER APPLICATION NUMBER: 1240/97
EARLIER FILING DATE: 1997-10-30
EARLIER FILING DATE: 1998-07-14
NUMBER OF EQ ID NOS: 58
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-183-412-9
                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-590-375-2 x US-09-183-412-9
FILING DATE: 1998-10-30
                                                                                                                                                                                                                                                                                                                                                            Quality: 2613.00
                                                                                                                                                                                                                                                                                                                                                                              Ratio: 5.421
Percent Similarity: 99.381
                                                                                                                                                                                                                           LENGTH: 1455
TYPE: DNA
COGANISM: Bacillus
US-09-183-412-9
                                                                                                                                                                                                                                                                                                                                            alignment_scores
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250 100 300 1117

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150 450 500

167

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184

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1451 AGCAA 1455

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GlyAspvalvalMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-13
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Gaps: 0
Percent Identity: 95.052
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                                                                                                         APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Nadersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, 1908-00
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                      Sequence 13, Application US/09183412
Patent No. 6204232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-183-412-13
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99.381
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                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Bacillus US-09-183-412-13
                                                                                             GENERAL INFORMATION:
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1001 CTCAGCCCGGGAAGCATTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050
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                                                                                                                                           151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
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117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 AACCATTCCAGCTTTAAGTGGCGCTGGTATCATTTTTGATGGGACAGATTG
                                                                                                                                                                                                                        pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG
                                                                                                                                                                                                                                         234 rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
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of No. 6297038th America, Inc.
                                                                                                                                                                                                                          1301 CAGGTGGTAACAAATGGATGTATGTGGGGAAAAATAAAGCGGGACAAGTT 1350
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-354-191A-4
                                                                 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Identity: 95.052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 62970380 No. 6297038disk of STREET: 405 Lexington Avenue, Suite 6400 STREET: New York STATE: New York COUNTRY: U.S.A. 121: 10174-6401 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09354191A
Patent No. 6297038
GENERAL INFORMATION:
APPLICANT: Bisgard Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4318.204-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent
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APPLICATION NUMBER: .08/600,656
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-590-375-2 x US-09-354-191A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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99.381
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                                                   TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACCTGCATGGAAGGGG 150
                                                                                                                                                                                                                                                                                  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
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                                                                                                     lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
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                                                                          euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                                                                                                                    yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
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from: 1
US-09-354-191A-4
 Align seg 1/1
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No. 59891690 No. 5989169disk of No. 5989169th America, Inc. 5 Lexington Avenue, 64th Floor
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                                                                                                                                                                                    erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
                                                                                                                                                                                                                                                             351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
                                                                                                          lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334
                                                                    901 TCTAATAGCGGTGGTTATTATGATATGAGAAATATTTTAAATGGTTCTGT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-600-908A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
851 GGAATCACTCGGTGTTTGATGTTCCTCTCCACTATAATTTGTACAATGCA
                                                                                                                                                                                                                                                                                                                                        367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
                                     SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59891690 No. 598916
STREET: No. 59891690 No. 64ti
CITY: New York
STATE: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08600908A Patent No. 5989169 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1458
                                                                                                                                                                                                                                                                                                                                                           95.052
                                                                                                                                                                                                                                                                                                                                                             Percent Identity:
                       FILING DAYE: L. L. CLASSIFICATION: A35
ATCHARSTETCATION: NAME: Green, Reza REGISTRATION NUMBER: 38 475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
TELEFAX: 212-878-9555
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nuclei acid
                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
        UMBER: US/08/600,908A
13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-600-908A-11
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-590-375-2 x US-08-600-908A-11
                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             Ratio: 5.421
Percent Similarity: 99.381
                                                                                                                                                                                                                                                                                                                                 Quality: 2613.00
             APPLICATION NUMBER:
                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: 1..1455
US-08-600-908A-11
                                                                                                                                                                                                              linear
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1000 1200 1001 CTCAGCCCGGGGAAGCATTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050 1051 CTTGCATATGCATTGGTTCTGACAAGGGAACAAGGTTATCCTTCCGTATT 1100 450 300 334 367 400 417 200 9 217 234 700 250 750 267 800 284 850 900 317 350 384 434 1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTTCCGGCTATGAAAT pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe 401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl 1151 417 1251 434 1301 1351 184 551 201 601 234 701 251 751 267 801 284 851 301 334 351 367 384 451 167

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SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrHisValArgAsnThrThrClyLysProMetPheAlaValAlaGluPh 267
                                                                                                                                                                                                                                                                                                                                                ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
                                                                                                                                          GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
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eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
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                                                                                                      euLysSerLysGly11eThrAlaValTrpI1eProProAlaTrpLysGly
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                          17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
           pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484
                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-683-838A-11
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Gaps: 0
Percent Identity: 95.052
                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    CITY: New YORK
STRATE: New YORK
COUNTY. United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"CMPUTER: Floppy disk
"CMPUTER: Floppy disk
                                                                                                                                                                                             APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/683,838A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
                                                                                                                                              seq_documentation_block:
    Sequence 11, Application US/08683838A
    Patent No. 6022724
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US-09-590-375-2 x US-08-683-838A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1458 base pairs TYPE: nucleic acid cypan bedness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 439
FELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
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Ratio: 5.421
nilarity: 99.381
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; LOCATION: 1..1
US-08-683-838A-11
                                                                                                                                                                     Patent No. 6022724
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New Yor
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Percent Similarity:
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MOLECULE TYPE:
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                                                                   ysGln 485
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No. 58245310 No. 5824531disk of No. 5824531th America
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                              erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                                                eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ottrup, Helle
APPLICANT: Bisgard-Frantzen, Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE, CULTON DATA:
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/446,803
FILING DATE: 01-June-1995
CLACKTFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrington, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 405 Lex:
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME:
                                                                                                                                                                                                                                                                                            401
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251 AATTGGAGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
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                                                                                                                                                                                                                                                                                 vaps: 0
Percent Identity: 86.598
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                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                  from: 1
               4157.204-US
            REFERENCE/DOCKET NUMBER: 4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-446-803-5
REGISTRATION NUMBER: 38,711
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US-09-590-375-2 x US-08-446-803-5
                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-08-446-803-5
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
                                                                                                                                                                 linear
                                                                                                                                                               TOPOLOGY:
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1251 AAATACCACGCATCCCAATTCAGGACTTGCGACTATCATGTCGGATGGGC 1300
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                                                                                                                                                                                                                                                                                                                                            317 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334
                                                                                                                                                                     751 ACCCATGTAAGAAACGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATT 800
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                                                          251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
                                                                                                rgileAspAlaValLysHisileLysTyrSerTyrThrArgAspTrpLeu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
                                                217 uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-5

ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America STREET: 405 Lexington Avenue 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe Length: 485 Gaps: 0 Percent Identity: 86.598 to: 1455 Patentin Release #1.0, Version #1.25 APPLICANT: Ottrup, Helle
APPLICANT: Bisgard Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Ostergaard, Peter Rabber
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
CORRESPONDENCE: 5
CORRESPONDENCE: 5 from: 1 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-JUNE-1995
ATTORNEY/AGENT INFORMATION: SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/861,837 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEPAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGHH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single Align seg 1/1 to: US-08-861-837-5 NAME: Harrington, James J. REGISTRATION NUMBER: 38,711 REFERENCE/DOCKET NUMBER: 41 alignment_block: US-09-590-375-2 x US-08-861-837-5 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-861-837-5 Floppy disk Quality: 2440.00 Ratio: 5.148 Percent Similarity: 97.732 ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy New York New York USA alignment_scores COUNTRY: CITY: 1 STATE: 101 34 51

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 84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
                                                                      134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
                                                                                                                                                                                                                                        151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 167
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                                                                                                                                                                                                                                                                                                                                                                                            GGAATCATTCTGTCTTTGATGTCCCCTTCATTATAATCTTTATAACGCG
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                                                                                                                                                                                                       1101 CTATGGTGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAG
                                                                                                                                                      434 roGlyGlyAsnLySTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                      451 TrpargaspileThrGlyAsnArgSerGlyThrValThrileAsnAlaAs
                                                       384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
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STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Lambitis, Elass J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0298
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MOLECULE TYPE: DNA (genomic)

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Gaps: 0
Percent Identity: 86.598
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US-09-590-375-2 x US-08-600-656-5
                            Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
US-08-600-656-5
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                                eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
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Ratio: 5.594
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-DB-N_Geneseq_1101_-QFMT-fastap_-SUFFIX_rng_-GAPOP=12.000
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                                                                                                Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
  OM of: US-09-590-375-2 to: N_Geneseq_1101:*
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Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent; starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance; alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent; dish-washing detergent; starch; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha-amylase. Alpha-amylase is an enzyme that acts on starch-related polysaccharides, hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit resistance to surfactants used in detergents, and decompose starch or starch-related polysaccharides in a highly random manner. The Bacillus species KSM-AR1378, from which this sequence was isolated, is an alkalophilic Bacillus strain. It was isolated from soil in the vicinity of the city of Tochigi. The enzyme is useful in improving the efficiency of dish-washing and laundry detergents, particularly on starch dirts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents the coding sequence for an alkaline liquefying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for removal of starch dirts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= alkaline liquefying alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - useful in
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Coding sequence for alkaline liquefying alpha-amylase.
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lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS
                             CGTACAAAAACACCCTATACATGCAGTCACATTGTTGTTGATAACCATGACT
                                                    erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                           erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
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  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
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                                                                       The present invention relates to a mutant alpha-amylase. Included in the invention are a gene encoding the mutant alpha-amylase, a vector containing the gene, and a transformed cell recombined by the vector. The enzyme is used in a detergent composition. The present sequence represents the mutant alpha-amylase gene.
                          in a detergent composition
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Gaps: 0
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                         mutant alpha-amylase for use
                                                  Example 1; Page 6-9; 12pp; Japanese.
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US-09-590-375-2 x AAC66234
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                                                                                                                                                                                                                                     GGACAGCTCCCACCCAAATTCAGGACTTGCAACTATATGTCCGATGGGC
                                                 rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                                                                   GAATCGATGCTGTGAAACATATTAAATACAGCTATACGAGAGATTGGCTA
                                                                                                                                                                                     eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                                                                                                                                                                             1148 TCTAATAGTGGTGGCTATTTTGATATGAGAAATATTTAAATGGTCTGT
                                                                                                                                                                                                                                                                                                                                     317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS
                                                                                                                                                                                                                                                                                                                                                              CGTACAAAAACACCCTATACATGCAGTCACATTTGTTGATAACCATGACT
                                                                                                                                                                                                                                                                                                                                                                                       erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                  yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1548 CAGGGGGTAATAAATGGATGTATGTCGGGAAACATAAAGCTGGCCAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 TrpArgAspileThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
                                                                                                                                                                                                                                                                                       SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
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101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACCTGCATGGAAGGGG 150

200

29

250

84

117 350 134 400 150 450 167 500 184 550 200 900 217 650

InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100

84

101 301 351 134 401 151 451

GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG luTyrThr11eGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG GGATCAGTCAGGCCTTCAAAACAAATATATAAATTCAGGGGAACAG

yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG

67

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This DNA sequence may be expressed recombinantly for the production of an alpha-amylase protein. The produced protein is characterized by having a specific activity at least 25% higher than the specific activity of Termanyl at 25-55 deg C and a pH of 8-10. The enzyme activity of Termanyl at 25-55 deg C and a pub of 8-10. The enzyme production of lignocellulosic materials, e.g. pulp, paper and cardboard from waste containing starch, for deinking recycled starch-coated, or starch containing printed paper, to modify starch for papermaking, for textile desizing, and beer-making
                                                                                                                                                                                                                                                                                                                                                                                                                                                        New alkaline Bacillus alpha-amylase - used in e.g. detergent compsns. starch liquefaction, textile desizing, starch modification
                                                                                                                             enzyme; EC-3.2.1.1; detergent; surfactant; textile;
                                                                                                                                                                                                                                                                                                                                                                           Rasmussen MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        Ostergaard PR, Outtrup H,
                                                                                                Bacillus sp. alkaline alpha-amylase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 48-49; 65pp; English.
seq_documentation_block:
ID AAT00776 standard; DNA; 1455 BP.
                                                                                                                                                                                                                                                                                    95DK-0000123.
94DK-0000353.
94DK-0001271.
                                                                                                                                                                                                                                                          95WO-DK00142
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                      Bisgard-frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-351318/45.
P-PSDB; AAR81835.
                                                                                                                                             beer; starch; ss.
                                                                                                                           Alpha-amylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beer making
                                                                                                                                                                                                 WO9526397-A1
                                                                                                                                                                                                                                                                                    03-FEB-1995;
29-MAR-1994;
                                                                                                                                                                                                                                                                                                                 03-NOV-1994;
                                                                                                                                                                                                                                                          29-MAR-1995;
                                                                    16-MAR-1996
                                                                                                                                                                                                                            05-0CT-1995
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                                        AAT00776;
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                                                                                                                                                                                                                 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334
rgIleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                               ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh
                                                                                                              rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                                                                                                                                                                       ACACATGTGCGTAACACCACAGGTAAACCAATGTTTGCAGTGGCTGAGTT
                                                                                                                                                                             SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                                                                     eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
       651
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51 34

euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly

17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34

from: 1 to: 1455

to: AAT00776

Align seg 1/1

alignment_block: US-09-590-375-2 x AAT00776

Length: 485 Gaps: 0 Percent Identity: 95.052

Quality: 2613.00 Ratio: 5.421 Percent Similarity: 99.381

alignment_scores:

50

234

LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA

551 201 601

217

501

167

184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr

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Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
1350
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                                                                                                                     1151 CTAAAATAGACCCTCTTCTGCAGGCACGTCAAACTTTTGCCTATGGTACG 1200
                                                                                                                                              417
                                                                                                                                                                                              434
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                                                                                                                                                                                                                                           434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX59632
                                                           1101 TTATGGGGATTACTACGGTATCCCAACCCATGGTGTTCCGGCTATGAAAT
                                                                                                                                                                                                                                                         1301 CAGGTGGTAACAAATGGATGTATGTGGGGAAAAATAAAGGGGGGACAAGTT
                                                                                                                                                                                                                                                                                          TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
                                                                                               erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                              yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                              GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nielsen BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a termamyl-like alpha-amylase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Termamyl-like alpha-amylase variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 91-92; 115pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            вр
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ID AAX59632 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98DK-0000936
97DK-0001240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .98WO-DK00471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borchert TV,
Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1998;
30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersen C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX59632;
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have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequences of the parent termamy1-like alpha-amylase: T141, K142, F143, D144, F145, P46, G147, R148, G149, O174, R181, G182, D183, G184, K185, A186, W189, S193, W195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K385, G456, W457, K458, P459, G460, T461, W462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.
                    specification describes termamy1-like alpha-amylase variants that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GCCAAATGACGGGAATCATTGGAACAGGTTGAGGGATGACGCAGCTAACT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACCTGCATGGAAGGGG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
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                                                                                                                                                                                                                                                                                                                   Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              Length: 485
Gaps: 0
Percent Identity: 95.052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1455
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Ratio: 5.421
Percent Similarity: 99.381
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US-09-590-375-2 x, AAX59632
                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                            LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
                                                                                                                                                                                                                                                                                                                                                                             eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpArgAsplleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
                                                                   GCAAGGCCTGGGACTGGGAAGTCGATACAGAGAATGGCAACTATGACTAT
                                  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
                                           rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                                                                                                              eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                                                                                                                                                                        rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                                                                                                                     ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh
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The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, F146, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, P267, W268, K269, W270, D271, L272, G273, A274, L275, K311, B346, K385, G456, W457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
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                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX59636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BR;
                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a termamyl-like alpha-amylase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 485
Gaps: 0
Percent Identity: 95.052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Termamyl-like alpha-amylase variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kjaerulff S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 98; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                          BP.
                                                                                                                                                                       AAX59636 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-DK00471.
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97DK-0001240.
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAX59636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.421 99.381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 2613.00
Ratio: 5.421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-590-375-2 x AAX59636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-326987/27
                                                                                                                                           seq_documentation_block
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   AGCAA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9923211-A1
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30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                        22-JUL-1999
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                                                                                                                                                                                                                                     AAX59636
1451
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17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL

ysgln 485

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Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Wild type Termamyl(RTM)-like alpha-amylase coding sequence #6.
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                                             951 GGTGCAAAAACATCCAACACATGCCGTTACTTTTGTTGATAACCATGATT 1000
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                                                                                                                                                                        434
                                                                                                                                                                                                                                     467
                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57597
               erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bisgard-Frantzen H, Borchert TV, Svendsen A;
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAX57597 standard; DNA; 1455 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97DK-0001172.
                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO-NORDISK AS.
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                                                                                                                                                                                                                                                                                                            1451 AGCAA 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus sp.
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                                                                                                                                                                                                                                                                                                                                                                       AAX57597;
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                                                                                                                                                        1201
                                                                                                           384
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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamy1-like alpha-amylase with a batha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. amyloliquefactiens or Bacillus spe #707. The Alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol). textile ${\tt lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr} \ 100$ yGlupheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG AGAGTTTAACCAGAAGGGGACGGTTCGTACAAAATATGGAACACGCAACC GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa lasnalaValGluValAsnArgSerAsnArgAsnGluGluIleSerGlyG 1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other; for Length: 485 Gaps: 0 Percent Identity: 95.052 or as detergents Disclosure; Page 83-84; 93pp; English from: 1 nseful desizing or starch liquefaction Ouality: 2613.00 Ratio: 5.421 Percent Similarity: 99.381 Align seg 1/1 to: AAX57597 alignment_block: US-09-590-375-2 x AAX57597 Variant alpha-amylases alignment_scores

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                                                                                                                                                                                                  roGlyGlyAsnLySTrpMetTyrValGlyLySHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                       lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS
                                                                                                                                                                                                                                                                                                       erGlnProGlyGluhlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                                                                                                                                                                                                  1001 CTCAGCCCGGGAAGCATTGGAATCCTTTGTTCAACAATGGTTTAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                              yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                              ThrHisValargAsnThrTlyLySPrOMetPheAlaValalaGluPh
                                                                                                      eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                                                                                                                                          SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
                                         CTTATGTATGCAGACGTGGATATGGATCACCCAGAAGTAATACATGAACT
                                                          uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
                                                                    rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417
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                                                                                                                                                                                     801
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                                                                                                                 701
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ysgln 485

184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr

pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG

ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr

to: 1455

to: AAA48480 from: 1

9

us-09-590-375-2.rng

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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one
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                                                                                                                                                                                                                                                                                                                                                                                Bacillus parent Termamyl-like alpha-amylase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bisgard-Frantzen H, Andersen
                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Termamyl-like alpha-amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant; enzyme stability; hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1455
/*tag= a
/product= "Termamyl-"
                                                                                                                                                                        ВР
                                                                                                                                    seq_documentation_block:
ID AAA48480 standard; DNA; 1455
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                                                                                                                                                                                                                                                                                                                (first entry)
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P-PSDB; AAY99602.
1451 AGCAA 1455
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                                                                                                                                                                                                                                        AAA48480;
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Gaps: 0 Percent Identity: 95,052 Length:

5.421 99.381

Percent Similarity:

alignment_block: US-09-590-375-2 x AAA48480

Quality: 2613.00

alignment_scores

Ratio

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550
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                                                                                                                                                                                                                                             84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
                                                                                                                                                                                                                                                                                             GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
                                                                                                                                                                                                                                                                                                                                                                     351 AAATGCGGTAGAAGTGAATCGGAGCAACCGAAACCAGGAAACCTCAGGAG 400
                                                                                                                      101 TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACCTGCATGGAAGGGG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
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1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17
                                                                                                                                                                                            184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801 TTGGAAAATGACCTTGGTGCAATTGAAAACTATTTGAATAAAACAAGTT
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                      1 CATCATAATGGAACAAATGGTACTATGATGCAATATTTCGAATGGTATTT
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                                                                                                euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                                                                                                                              ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl
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                                                                                                                                                        eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48485
      SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                       317 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS
                                                                              334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                       901 TCTAATAGCGGTGGTTATTATGATATGAGAAATATTTAAATGGTTCTGT
                                                                                                                   351 LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
                                                                                                                                                                                                                                                                                                      417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                                                                                                                           TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Termamyl-like alpha-amylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant; enzyme stability; hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus Termamyl-like alpha-amylase DNA sequence #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAA48485 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= /
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA48485;
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WO200029560-A1

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The present sequence encodes an alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacilius genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and textile desizing. Hybrid alpha-amylases comprising partial and ocid sequences derived from two or more alpha-amylases have also been created
                                                                                                                                                                                                                                                                                                          Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1455 BP; 461 A; 248 C; 361 G; 385 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Length: 485
Gaps: 0
Percent Identity: 95.052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAA48485 from: 1 to: 1455
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 69-70; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in order to increase enzyme stability
                                                                                                    98DK-0001495
                                                                                                                                                                                                        Kjaerulff S,
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US-09-590-375-2 x AAA48485
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Percent Similarity:
                                              16-NOV-1999;
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25-MAY-2000,
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1201 CAGCATGATTACTTTGATCATCATGATATTATCGGTTGGACAAGAGAGGG 1250
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GGTGATGTCGTCATGAATCATAAAGGTGGAGCAGATGGTACGGAAATTGT 350
                                                                                                                                                                                                          pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
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                                                                                                                                                                lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                            AAATGCGGTAGAAGTGAATCGGAGCAACCGAAACCAGGAAACCTCAGGAG
                                                                                      luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn
                                                                                                      ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamy1-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis, a mayloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing starch liquefaction (e.g. for production of sweeteners or ethanol). Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss. Wild type Termamyl(RTM)-like alpha-amylase coding sequence #1. textile 1350 TGGAGAGATATTACCGGAAATAGGACAGGCACCGTCACAATTAATGCAGA 1400 467 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57592 TrpArgAsp11eThrGlyAsnArgSerGlyThrValThr11eAsnAlaAs roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal Sequence 1455 BP; 463 A; 246 C; 361 G; 385 T; 0 other; for detergents or à Disclosure; Page 76-77; 93pp; English as Borchert TV, useful BP desizing or starch liquefaction seq_documentation_block:
ID AAX57592 standard; DNA; 1455 98WO-DK00444 97DK-0001172 (first entry) (NOVO) NOVO-NORDISK AS. Variant alpha-amylases Bisgard-Frantzen H, WPI; 1999-277632/23 1451 AGCAA 1455 ysGln 485 WO9919467-A1 13-OCT-1998; 13-OCT-1997; 16-JUL-1999 alignment_scores: Bacillus sp. 22-APR-1999 AAX57592; 1301 451 1351 484 434

Length:

Quality: 2601.00 Ratio: 5.396

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284
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AACCATTCCAGCTTTAAGTGGCGCTGGTATCATTTTGATGGGACAGATTG
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                                                                                                                                                         yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
                                                                                                                                                                                            lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
                                                                                                     euLysSerLysGly11eThrAlaValTrp11eProProAlaTrpLysGly
                                                HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
94.433
Identity:
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                                   to:
 Percent
                                   from: 1
                                   to: AAX57592
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                     US-09-590-375-2 x AAX57592
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Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
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                                                                                           lvalGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334
                                     900
                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX59633
                                                                                                                                                                                                       TrpArgAsp1leThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                                                                                                                                                                                                                                                                                                                        roglyglyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                   LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
                                                                                                                                                                                                                                            erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                                                                                      GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
301 TTGGAAAAATGACCTTGGTGCAATTGAAAACTATTTGAATAAAACAAGTT
                            284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a termamyl-like alpha-amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAX59633 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ysGln 485
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184

217

13

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lyLysalaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                     351 TCTTGCTGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGG
                                                                                                                      luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn
                                                                                                                                                  ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
                                                                                                                                                                                                                                                                 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTCGATGGTGTAGATTG
                                                                                                                                                                                                                                                                                                                pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAAGGCATGGGATTGGGAAGTAGATTCGGAAAATGGAAATTATGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
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                                                                                                                                                                                                                                                                                                                                                                                                         184
                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, A186, F145, P146, G147, R148, G149, Q174, R181, G182, D183, Q184, K185, A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, E346, K385, G456, N457, K458, P459, G460, T461, V462, A274, L275, K311, E346, K385, G456, N457, K458, P459, G460, T461, V462, G450, The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the variants of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other
                                                                                                                                                                                                                  S, Nielsen BR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 485
Gaps: 0
Percent Identity: 86.598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0
                                                                                                                                                                                                                                                                                                                                    New Termamyl-like alpha-amylase variants
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 92-93; 115pp; English.
                                                                                                                                                                                                               Kjaerulff
                                               98WO-DK00471
                                                                                              98DK-0000936
                                                                                                                 97DK-0001240
                                                                                                                                                                                                             Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
                                                                                                                                                                (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                      Svendsen A;
                                                                                                                                                                                                                                                                                     WPI; 1999-326987/27
                                                                                                                 30-OCT-1997;
                                               30-0CT-1998
                                                                                                                                                                                                             Andersen C,
14-MAY-1999
                                                                                           14-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                      Nissen TL,
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250

267

801

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GGAATCATTCTGTCTTTGATGTCCCCCTTCATTATAAATCTTTATAACGCG 900
                                                           erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                                                                                        rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                                SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                                                              lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS
                                                                                                                                                                                          LeuAlaTyrAlaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
                                                                                                                                                                                                                                           eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
                                                                                                                                                                                                                                                                                         erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                              317
                                                                                                                     951
                                                                                                                                            334
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284
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150

67

200

201 84 251 101

67

lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr

GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa

117

34 101 21 151

ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl ACTICGCAAAATGATGTGGGGGTATGGAGCCTATGATCTTTATGATTTAGG

from: 1 to: 1455

Align seg 1/1 to: AAX59633

alignment_block: US-09-590-375-2 x AAX59633

367

us-09-590-375-2.rng

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes termanyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants have altered amino acid sequences to improve properties. The variants amino acid sequence of the parent termanyl-like alpha-amylase: T141, K142, F143, D144, F145, P46, G147, R148, G149, Q174, R181, G182, D183, G184, K185, A186, W189, S193, M195, H107, K108, G109, D166, W167, D168, A274, L275, K311, E346, K35, G456, W457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweetners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present sequence encodes an amylase that can function as the parent sequence in the production of the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
                                                                                                                                                                    467
yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX59637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 403 T; 0 other;
                                                                                                              451 TrpArgAsplleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nielsen BR
                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a termamyl·like alpha·amylase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Termamyl-like alpha-amylase variants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 99; 115pp; English.
                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAX59637 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-DK00471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DK-0000936
97DK-0001240
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                                                                                                                                                                                                                                                            1451 AACGA 1455
                                                                                                                                                                                                                                 ysgln 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09923211-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                          AAX59637;
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650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 267
                                                                                                                                                                                                                                                                                                                               400
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                                                                                                                                                                                                                                                                                                                                                                                PASPGINSETARGGINLEUGINASNIYSIIETYRIYSPHEARGGIYTHRG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900
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                                                                                                                                                                                                           lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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                                                                                                                                                                                                                                                      GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGAAGATGGGAGAATGGTATACAAATACATTAAATCTTGATGGATTTA
                                                                                                                                                                                                                                                                                                                                                lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                                                                                                                                                                                                                                                                         1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
                                                                                                           17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL
                                                                                   Length: 485
Gaps: 0
Percent Identity: 86.598
                                                           to: 1455
                                                           from: 1
                                                           to: AAX59637
Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
                                           US-09-590-375-2 x AAX59637
                                   alignment_block:
                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551
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textile

for

or

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Svendsen

7.2

751 267 284 851 301 901

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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamyl-like alpha-amylase with a variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in WO9526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 485
Gaps: 0
Percent Identity: 86.598
                                                                                                                                                                                                                                                                                       useful as detergents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 1455
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 77-78; 93pp; English
                                                                                                                                                                                                                    ΤV,
                                                                                                                                                                                                                                                                                       Variant alpha-amylases - usefuidesizing or starch liquefaction
                                                                                                                                                                                                                        Borchert
                                                                                                                    98WO-DK00444.
                                                                                                                                                     97DK-0001172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-590-375-2 x AAX57593
                                                                                                                                                                                      (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                      Bisgard-Frantzen H,
                                                                                                                                                                                                                                                      WPI; 1999-277632/23
                                                                                                                    13-OCT-1998;
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                                                 W09919467-A1
                 Bacillus sp
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 Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wild type Termamyl(RTM)-like alpha-amylase coding sequence #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1351 TGGCATGACATAACTGGAAATAAACCAGGAACAGTTACGATCAATGCAGA 1400
                                                                                                                                                                                                                                                                                                                                                                                        367
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rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
                                                                                                                                                                                 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
                                                                                                                                                                                                                                                                                                                       erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1301 CAGGGGGAGAAATGGATGTACGTACGCAAAATAAAGCAGGTCAAGTT
                                                                  GGAATCATTCTGTCTTTGATGTCCCCCTTCATTATAATCTTTATAACGCG
                                                                                                                                                                                                      LeualaTyralaLeuIleLeuThrArgGluGlnGlyTyrProSerValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                          eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpArgAspileThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                                  eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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ID AAX57593 standard; DNA;
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us-09-590-375-2.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434
                              TCTTGCTGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGG
                                                                                                                             lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
                                                                                                                                                                                                                                                                    317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS
                                                                                                                                                                                                                                                                                                                                                                                                                       erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                              PASPGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG
                                                                                                                                                                                            uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
                                                                                                                                                                                                                                                          ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh
                                                                                                                                                                                                                                                                                          eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                                                                                                                                                                                                                                                                   erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
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117
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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamy1-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W0526597, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus spe #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sweeteners or ethanol).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                        Wild type Termamyl(RTM)-like alpha-amylase coding sequence #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                textile
                                                                                                                                                                           467
                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57598
pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL
                                                                                                  TrpArgAspIleThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs
                                          roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 485
Gaps: 0
Percent Identity: 86.598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - useful
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                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAX57598 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-DK00444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DK-0001172.
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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97.732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variant alpha-amylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-277632/23
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                               1451 AACGA 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp.
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                                                                                     uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL||||||||||||||:::||||
                                                                                                                                                                                                                101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa
                                                                                                                                                                                                                                                                                             1AsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                                                                                                                                                                                                                                                                                  184 lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAAGGCATGGGATTGGGAAGTACGGAAAATGGAAATTATGATTAT
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                                                                                                                                                                                                                                                                                                                                                                                151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
                             to: 1455
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                             from:
                            AAX57598
alignment_block:
US-09-590-375-2 x AAX57598
                             to:
                            Align seg 1/1
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TGGATGGGCTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGA 1450
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                                              317
                                                         Bacillus parent Termamyl-like alpha-amylase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48481
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/product= "Termamyl-like alpha-amylase"
                                                                                                                                                                                        317 lValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS
                                                                                                                                            erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro
                                                                                                                                                                                                                                                                                                                                                                                     417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                     roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla
                                              SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa
                                                                                                                                                                                                                                                                                         erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
                                                                                                                                                                                                                                                                                                                                        GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl
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ID AAA48481 standard; DNA; 1455
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251

101

GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa

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The present sequence encodes a parent Termamyl-like alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by rariants are suitable for the industrial processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for warning, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more
                                                                                                                                                                                                                                                                                                           one
                                                                                                                                                                                                                                                                                       Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in or more solvent exposed amino acid residues
                                                                                                                                                                                                        Andersen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 352 G; 403 T; 0 other;
                                                                                                                                                                                                    Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 66-67; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1455 BP; 473 A; 227
                                                                                                   99WO-DK00628
                                                                                                                                     98DK-0001495
                                                                                                                                                                                                        Kjaerulff S,
                                                                                                                                                                      (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                       WPI: 2000-38777/33
                                                                                                                                                                                                                                                         P-PSDB; AAY99603
                                WO200029560-A1
                                                                                                                                     16-NOV-1998;
                                                                                                                                                                                                          Svendsen A,
                                                                                                   16-NOV-1999;
                                                                  25-MAY-2000
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GCCTAATGATGGGAATCACTGGAATAGATTAAGAGATGATGCTAGTAATC 100
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                                                                                                                                                                                               34
                                                                                                                                       1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
                                                                                                                                                      uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL
                                                                                                                                                                                                                                                        euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                                                                                                                                                                                                                                                                                               ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl
                                     Percent Identity: 86.598
            Length:
                                                                                                            to: 1455
                                                                                                             from: 1
                         5.148
97.732
                                                                                                            Align seg 1/1 to: AAA48481
          Quality: 2440.00
                                                                                 US-09-590-375-2 x AAA48481
                           Ratio:
Percent Similarity:
alignment_scores:
                                                                   alignment_block
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84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100

84

ACTICGCAAAATGATGTGGGGTATGGAGCCTATGATCTTTATGATTTAGG

151

201

1100 1150 951 TGTTCAAAAGCATCCAATGCATGCCGTAACTTTTGTGGATAATCACGATT 1000 350 367 400 450 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300 950 400 167 200 9 217 650 234 267 800 284 850 900 317 334 117 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150 ACATACTCAGACTTTAAATGGCGTTGGTATCATTTCGATGGTGTAGATTG 500 pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro LeuAlaTyrAlaLeuIleLeuThrArgGluGluGlnGlyTyrProSerValPh eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS erLysIleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT CTTGCTTATGCGCTTATTTTAACAAGAGAACAAGGCTATCCCTCTGTCTT GGAATCATTCTGTCTTTGATGTCCCCCTTCATTATAATCTTTATAACGCG 317 lValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa lyLysAlaTrpAspTrpGluValAspIleGluAsnGlyAsnTyrAspTyr LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 1001 1051 351 134 101 451 501 184 201 217 651 234 701 251 267 801 284 851 301 901 351 367 384 151 167 551 601

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genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed estables may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AATTGGAGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pAspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAspAlaAlaAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 InLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe
                                                                                                                                                                                                                                                                                                                     Length: 485
Gaps: 0
Percent Identity: 86.598
                                                                                                                                                                                                                                           Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1455
                                                                                                                                                                                                      order to increase enzyme stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                   Quality: 2440.00
Ratio: 5.148
Percent Similarity: 97.732
                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: AAA48486
                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-590-375-2 x AAA48486
                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501
    The present sequence encodes a parent alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues
                                                                                                                                                                                                                                                                                                                   1400
                                       1151 CCAAGATTGATCCAATCTTAGAGGCGCGTCAAAATTTTGCATATGGAACA 1200
                                                                                                                                                                                                                                                                                                                                                                             ပဲ
                                                                                                                                                                                                                                                                                                                                                          484
                                                                                                                                                                                                 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
                                                                                                                                                                                                                                                                            451 Trp&rgAspileThrGlyAsnArgSerGlyThrValThrIleAsnAlaAs 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48486
                                                                                                                                                                                                                                                                                                       pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Termamyl-like alpha-amylase"
                                                                                                                     yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant; enzyme stability; hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus Termamyl-like alpha-amylase DNA sequence #4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bisgard-Frantzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 70-71; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA48486 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-DK00628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-387777/33.
P-PSDB; AAY99609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200029560-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1451 AACGA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                      484 ysGln 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA48486;
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                                                                                                                   417
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200

67

34

other

100

350

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650
                                                                                                                              234
                    SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317
                                                                                                   eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS 384
                                                                                                                                                                                                                             434 roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 450
                                                                                                                                                                                                                                                467
uArgAsnTrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA
                                                                                                                                                                                                                                             451 TrpargaspileThrGlyasnargSerGlyThrValThrIleAsnalaas
                                                                                                                                                                                                                                                                              ysGln 485
               217
                               234
                                       701
                                               251
                                                       751
                                                               267
                                                                       801
                                                                               284
                                                                                       851
                                                                                               301
                                                                                                                                                              367
                                                                                                                                                                                                                                                                             484
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AACGA 1455

us-09-590-375-2.rng

us-09-590-375-2.rge

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A23402 B.licheniformis gene
A27772 Alpha amylase coding
A47677 Sequence I from Pate
A11930 Alpha amylase gene.
I24553 Sequence 33 from pat
                                                                                                                                                                                                          seq_documentation_block:
LOCUS E12445
DEFINITION DNA encoding liquefaction type alkaline alpha amylase from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1...14

145. .1695

/product-'Liquefaction type alkaline alpha FT

amylase from

Bacillus sp.'

1696. .1776

.re 1..31

/note-'Signal sequences'

.re 127. .132

/note-'SD sequences'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp.
JP 1996336392-A/1
JP 2006336392-A/1
14-DEC-1995 JP 1995147257
HATADA YUUJI, OZAKI KATSUYA, ARA KATSUTOSHI, KAWAI SHUJI,
                                                                                                                                                                                                                                                                                                                 E12445
E12445.1 GI:3251278
JP 196336392-A/1.
Bacillus sp.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 1776)
Hatada, Y., Ozzki, K., Ara, K., Kawai, S. and Ito, S. LIQUEFIED-TYPE ALKALI ALPHA-AMYLASE GENE
Patent: JP 1996336392-A 1 24-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Bacillus
/strain='KSM-AP1378'
/clone='pAML100'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
     1.0e-130
1.0e-130
1.1e-130
1.3e-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:1409"
305 c 417 g 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1776
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1. 1776
/organism="Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CI2NI5/09,CI2N9/28;
strandedness: Double;
topology: Linear;
hypothetical: No;
anti-sense: No;
     2495.46
2495.46
2494.95
2493.75
2493.75
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  + 1909.00
+ 1909.00
+ 1909.00
+ 1909.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 2713.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -35_signal
-10_signal
-10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -35_signal
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US-09-590-375-2 x E12445
                                                                                                                                                                   seq_name: gb_pat:E12445
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OS Bacil

PD 24-DD

24-DD 24-DD

24-DD 24-DD

110 SUSCUM

PC C12N

CC STCA

CC APPO

CC APPO
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gb_pat:A23402
gb_pat:A27772
gb_pat:A47677
gb_pat:A17930
gb_pat:I24553
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                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E12445 DNA encoding liquefacti
AB008763 Bacillus sp. gene for
AR027254 Sequence 4 from pater
AR049517 Sequence 4 from pater
AR129912 Sequence 9 from pater
AR139912 Sequence 9 from pater
AR139913 Sequence 9 from pater
AR137883 Sequence 9 from pater
AR137817 Sequence 13 from pater
AR143217 Sequence 13 from pater
AR037255 Sequence 11 from pater
AR047255 Sequence 5 from pater
AR049518 Sequence 5 from pater
AR129918 Sequence 10 from pater
AR139918 Sequence 10 from pater
AR139918 Sequence 10 from pater
AR13788 Sequence 10 from pater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M18862 Bacillus sp. (alkalophi
AX036928 Sequence 1 from Pater
AX037043 Sequence 3 from Pater
AX037042 Sequence 3 from Pater
AX037040 Sequence 1 from Pater
AX037040 Sequence 1 from Pater
AX037040 Sequence 1 from Pater
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B.stearothermophilus DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U22045 Bacillus sp. álpha-amyl
E12201 DNA encoding a heat-and
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                                                                                                                                                                                                     -WODEL-frame-promodel -DEV-x1h
-Q-Cgn2_1/USPTO_spool/US09590375/runat_28112001_152037_21059/app_query.fasta_1.1092
-Q-Cgn2_1/USPTO_spool/US09590375/runat_28112001_152037_21059/app_query.fasta_1.1092
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AR143215 Sequence 11 from pt
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                                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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1 HisHisAsnGlyThrAsnGlyThrMetMetG 	/ uProAsinAspClyAsnHisTrpAsnArgLeuArgAspAspAlaAsnL 	4 euLysSerLysGlylleThrAlaValTrpIleProProAlaTrpLysGl; 	1 ThrSerGlnasnaspValGlyTyrGlyalaTyraspLeuTyraspLeuG: 	67 yGlupheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSer/ 	84 InLeugInGiyalaValThrSerLeuLysAsnAsnGlyile 	1 GlyaspValValMetAsnHisLysGlyGlyalaaspGlyThrGluMetV. 	7 lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGly	lufyrThrileGlualafrpThrLysPheaspPheProGlyArgGlyAsn 	ThrhisSerasnpheLysTrpargTrpTyrHisPheaspGlyThraspTr 	PASPG1nSerArgG1nLeuG1nAsnLysI1eTyrLysPheArgG1yThr(YLYSA aTrpAspTrpGluVa AspIleGluAsnGlyAsnTyr. 	LeuwetTyralaaspileaspwetaspHisProGluvalIleasnGlule 	uargasntrpglyValtrpyrthrasnthreudsnLeudspG 	rgileaspalavallyshisilelysfyrSerfyrfhrargasptr 	ThrHisValargAsnThrThrGlyLysProMetPhealaValala	eTrplysasnaspLeualaalaileGluasnTyrLeuasnLysThrSer' 	rpAsnHisSerValPheAspValProLeuHisTyr

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Bacillus sp. (strain:KSM-1378) DNA.
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Bacillus sp. gene for amylase, complete cds.
AB008763
AB008763.1 GI:3445479
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DEFINITION BACILLUS SP. 9
ACCESSION AB008763.1 GI
VERSION AB008763.1 GI
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                          eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
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  ACCCATTCCAACTTTAAATGGCGCTGGTATCATTTTGATGGGACAGATTG
                                                                                                                                  LeuMetTyrAlaAspIleAspMetAspHisProGluValIleAsnGluLe
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Location/Qualiflers
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Ratio: 5.594
Percent Similarity: 100.000
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Gaps: 0
Percent Identity: 95.052
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Sequence 4 from patent US 56
AR027254 AR027254.1 GI:5938094
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101 GlyaspvalvalMetasnHisLysGlyGlyalaAspGlyThrGluMetva 117	117 lasnalaValGluValAsnargSerasnargasnGlnGluIleSerGlyG 134 	134 luTyrThrIleGlualaTrpThrLysPheaspPheProGlyargGlyasn 150 :::	151 ThrhisSerasnPheLysTrpargTrpTyrHisPheaspGlyThraspTr 167 :::	167 paspGinSerargGinLeuGinAsnLysIleTyrLysPheargGlyThrG 184	184 lyLysalaTrpaspTrpGluValaspIleGluAsnGlyAsnTyrAspTyr 200 	201 LeuWetTyralaaspileAspWetaspHisProGluValIleAsnGluLe 217	217 uargasnTrpGlyValTrpTyrThrasnThrLeuAsnLeuAspGlyPhea 234	234 rglleaspalavalLysHisIleLysTyrSerTyrThrargaspTrpLeu 250 	251 ThrhisvalargasnThrThrGlyLysProMetPhealavalalaGluPh 267	267 eTrpLysAsnAspLeuAlaalaIleGluAsnTyrLeuAsnLysThrSerT 284 	284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300 	301 SerAsnSerGlyGlyTyrPheAspMetArgAsnIleLeuAsnGlySerVa 317 	317 lvalglnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 334	334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLySPro 350	351 LeualaTyralaLeuIleLeuThrargGluGluGlyTyrProservalPh 367 	367 eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLyss 384	384 erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 400	401 GlnHisAspTyrPheAspHisHisAspIleIleGlyTrpThrArgGluGl 417
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CTTGCATATGCATTGGTTCTGACAAGGGAACAAGGTTATCCTTCCGTATT 1100
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                                                                         |InLeuGlnGlyalaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
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|AGCTACAGGCTGCGGTGACCTCTTTAAAAATAACGGCATTCAGGTATAT
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95.052
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Bigs, ang.rd-Frantzen, H., Svendsen, A. and
Amylase variants
Patent: US 6093562-A 4 25-JUL-2000;
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248 c 361 q
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Sequence 4 from patent US
AR104348
AR104348.1 GI:12817056
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Percent Similarity: 99.381
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US-09-590-375-2 x AR104348
                                                                                                                                                                                                                                                                                seq_name: gb_pat:AR104348
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LOCUS AR104348
                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
Unclassified.
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Unknown.

KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION VERSION

461

BASE COUNT ORIGIN

source

FEATURES

TITLE

REFERENCE AUTHORS alignment_scores

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ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl
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Svendsen.A., Borchert.T.Vedel and Bisg.ang.rd-Frantzen,H.
.alpha.-amylase mutants
Patent: US 6187576-A 9 13-FEB-2001;
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                 1151 CTAAAATAGACCCTCTTCTGCAGGCACGTCAAACTTTTGCCTATGGTACG
                                                          1201 CAGCATGATTACTTTGATCATCATGATATTATCGGTTGGACAAGAGAGGG
                                                                                                                               roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal
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Gaps: 0
Percent Identity: 95.052
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248 c 361 q
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AR129912. GI:14117809
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US-09-590-375-2 x AR129912
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Unclassified.
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FEATURES
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TITLE
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SOURCE
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CTCAGCCCGGGGAAGCATTGGAATCCTTTGTTCAACAATGGTTTAAACCA 1050
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TrGGAAAATGACCTTGGTGCAATTGAAAACTATTGAATAAAACAAGTT
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lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
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AAATGCGGTAGAAGTGAATCGGAGCAACCGAAACCAGGAAACCTCAGGAG 400
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TTGGAAAATGACCTTGGTGCAATTGAAACTATTGAATAAAACAAGTT
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                        euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
                                               TAAAGAGTAAAGGGATAACAGCTGTATGGATCCCACCTGCATGGAAGGGG
                                                                                                                       yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
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Svendsan, A. Borchert, T. Vedel and Bisg.ang.rd-Frantzen, H.
alpha.-amylase mutants
alpha. 18 6187576-A 14 13-FEB-2001;
                                                                                    TTATGGGGATTACTACGGTATCCCAACCCATGGTGTTCCGGCTATGAAAT 1150
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                                       eTyrGlyAspTyrTyrGlyIleProThrHisGlyValProSerMetLysS
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AR129917
AR129917.1 GI:14117814
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US-09-590-375-2 x AR129917
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484

DEFINITION ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS 250

750 267 800 284

700

850 300 900 317

alignment_scores

source

JOURNAL

TITLE

FEATURES

BASE COUNT ORIGIN

us-09-590-375-2.rge

1 HisHisAsnGlyThrAsnGlyThrMetMetGlnTyrPheGluTrpHisLe 17	. 17 uProAsnAspGlyAsnHisTrpAsnArgLeuArgAspAlaAlaAsnL 34	34 euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly 56	51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl 67 	67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84	84 InLeuGlnGlyAlaValThrSerLeuLySASnAsnGlyIleGlnValTyr 10	101 GlyaspvalvalmetasnHisLysGlyGlyalaAspGlyThrGluMetVa 11	117 lasnalavalGluValasnargSerasnargasnGlnGluIleSerGlyG 13	134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 15 :::	151 ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr 16 :::	167 paspGlnSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 1E	184 lyLysalaTrpaspTrpGluValaspIleGluAsnGlyAsnTyrAspTyr 2C	201 LeuwetTyralaaspileaspwetasphisProGluvalileasnGluLe 21	217 uargasnfrpGlyValTrpTyrThrAsnThrLeuAsnLeuAspGlyPheA 2: 	234 rglleAspAlaValLySHisIleLySTyrSerTyrThrArgAspTrpLeu 2: 	251 ThrHisValArgAsnThrThrGlyLysProWetPheAlaValAlaGluPh 26 	267 eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT 26	284 rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 3(0. Constant to to the section of the
334 erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 350	LeualaTyralaLeuIleLeuThrargGluGlnGlyTyrProSerValPh 367 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	eTyrGlyAspTyrTyrGly1leProThrHisGlyValProSerMetLysS 38	erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr 40	GlnHisAspTyrPheAspHisHisAspTileIleGlyTrpThrArgGluGl	SerAspGlyP 4 	roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal [Hill	TrpargaspileThrGlyAsnargSerGlyThrValThrIleAsnalaAs TGGAGATATTACGGAAATAGGACAGCACGTCACAATTAATGCAGA		ysgln 485 - - - - -		Aed_documentation_block: LOGUS LOCUS BERINITION Sequence 9 from patent US 6197565. VECESSION AR137883 VERSTON AR137883	Unknown.	REFERENCE 1 (bases 1 to 1455) AUTHORS Svendsen, A., Kjaerulff, S., Bisgaard-Frantzen, H. and Andersen, C. TITLE alpha-Amylase variants TOTHER AUTHORS A CONTRACT OF TOTAL OF TOTAL OF TOTAL OF TOTAL OF TOTAL OF TOTAL OF T	SS Location/Qualifiers U. 1455 1. 1455 / Organism="unknown" 121.2"		Description 1 Percent Similarity: 99.381 Percent Identity: 95.052	k: -2 x AR137883	Align seg 1/1 to: AR137883 from: 1 to: 1455

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                           leThrAlaValTrpileProProAlaTrpLysGly 50
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Svendsen,A., Kjaerulff,S., Bisgaard-Frantzen,H. and Andersen,C.
alpha.-Amylase variants.
Patent: US 6197565-A 13 06 MAR-2001;
Location/Qualifiers
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US-09-590-375-2 x AR143213
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Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B., Nissen,T.Lauesgaard and Kj.ae butted.rulff,Sslashedren.alpha.-anlase mutants
Patent: US 6204232-A 9 20-MAR-2001;
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Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B.,
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                                                                                                    rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 300
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                                                eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
                                                             erLyslleAspProLeuLeuGlnAlaArgGlnThrTyrAlaTyrGlyThr
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LOCUS
AR143217
DEFINITION Sequence 13 from patent
ACCESSION AR143217
VERSION AR143217.1 GI:15104503
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Unclassified.
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Nissen, T. Lauesgaard and Kj.ae butted.rulff, Sslashedren
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                                                                                                             Length: 485
Gaps: 0
Percent Identity: 95.052
         .alpha.-amlase mutants
Patent: US 6204232-A 13 20-MAR-2001;
                                                                                                                                                                                       to: 1455
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                                               /organism="unknown"
1 248 c 361 g
                            Location/Qualifiers
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                                                                                                                                                       alignment_block:
US-09-590-375-2 x AR143217
                                                              Q
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Ratio:
Percent Similarity:
                                                           461
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Borchert, T. Vedel

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luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150
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Gaps: 0
Percent Identity: 95.052
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Svendsen,A., Blsg. and rd Frantzen,H.
alpha -amylase mutants
Patent: US 5989169-A 11 23-NOV-1999;
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                                                                                                           Location/Qualifiers
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248 c 361 a
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 GI:10014319
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Ratio: 5.421
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US-09-590-375-2 x AR087556
                                  Unknown.
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                                    rgileAspAlaValLysHisileLysTyrSerTyrThrArgAspTrpLeu
                                                            701 GAATAGATGCAGTGAAACATATAAAATATAGCTTTACGAGAGATTGGCTT
                                                                                     ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh
                                                                                                                                    eTrpLysAsnAspLeuAlaAlaIleGluAsnTyrLeuAsnLysThrSerT
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LOCUS AR087556 1458 bp DNA
DEFINITION Sequence 11 from patent US !
ACCESSION AR087556
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1 (bases 1 to 1455)
Outtrup, H., Bisg ang.rd-Frantzen, H., stergaard, P.Rahbek, Rasmussen, M.Dolberg and Van Der Zee, P.
Alkaline bacillus amylase
Patent: US 5856164-A 5 05-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyAspValValMetAsnHisLysGlyGlyAlaAspGlyThrGluMetVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lAsnAlaValGluValAsnArgSerAsnArgAsnGlnGluIleSerGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CATCATAATGGGACAAATGGGACGATGATGCCAATACTTTGAATGGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euLysSerLysGlyIleThrAlaValTrpIleProProAlaTrpLysGly
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                                                                                                                                                                                                                                                                                         Length: 485
Gaps: 0
Percent Identity: 86.598
                                     PAT
                                                                                                                                                                                                                                                                                                                                                                            to: 1455
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                                               5856164
                              DNA
US F
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1. .1455
                                                                                                                                                                                                                /organism="unknown"
227 c 352 q
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                                   ARU2/255 1455 bp
Sequence 5 from patent
                                                                      AR027255.1 GI:5938095
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5.148
97.732
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gb_pat:AR027255
                                                                                                                     Unclassified
                       seq_documentation_block:
LOCUS AR027255
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Ratio:
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                                                                                               Unknown.
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                                              DEFINITION
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                                                            ACCESSION
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paspGlnSerargGlnLeuGlnasnLysIleTyrLysPheargGlyThrG 	lytysalaTrpaspTrpGluValaspIleGluAsnGlyasnTyrAspTyr 	LeuMetTyralaAspIleAspMetAspHisProGluValIleAsnGluLe 	uArgasnTrpGlyValTrpTyrThrAsnThrLeuasnLeuaspGlyPhea ::	rg1leAspAlaValLysHis1leLysTyrSerTyrThrArgAspTrpLeu 	ThrHisValArgAsnThrThrGlyLysProMetPheAlaValAlaGluPh 	eTrpLysasnaspLeualaalalleGluasnTyrLeuasnLysThrSerT 	rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 	SerasnSerGlyGlyTyrPheaspMetargasnIleLeuasnGlySerVa 	1ValGlnLysHisProIleHisAlaValThrPheValAspAsnHisAspS 	erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 	LeualaTyralaLeu11eLeuThrargGluGlnGlyTyrProSerValPh 	eTyrGlyaspTyrTyrGlylleProThrHisGlyValbroSerNetLysS 	erlysileaspProLeuLeuGinalaargGlnThrTyralaTyrGlyThr :: CCAAGATTGATCCAATCTTAGAGGCGCGTCAAAATTTTGCATATGGAACA	GIBHISASPTYrPheASPHISHISASPILEILEGLYTrpThrargGluGl 	yaspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP ::::::::	roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal 	Trpargasp11eThr61yasnargSer61yThrVa1Thr11easna1aas :::	pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL
9	184	201 601	217 651	234 701	251 751	267 801	284 851	301 901	317 951	334	351 1051	367 1101	384 1151	401 1201	417	434	451 1351	467

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29-SEP-1999
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Outtrup, H., Bisg ang.rd-Frantzen, H., stergaard, P.Rabbek,
Rasmussen, M.Dolberg and Van der Zee, P.
Alkaline bacilus amylase
Patent: US 5824531-A 5 20-OCT-1998;
Location/Qualifiers
1. 1455
1401 TGGATGGGCTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lnLeuGlnGlyAlaValThrSerLeuLysAsnAsnGlyIleGlnValTyr 100
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                                                                                                                  PAT
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Gaps: 0
Percent Identity: 86.598
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Sequence 5 from patent US 5824531.
AR049518 1 GI:600557
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Ratio: 5.148
Percent Similarity: 97.732
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US-09-590-375-2 x AR049518
                                                                               seq_name: gb_pat:AR049518
                                                                                                   seg_documentation_block:
LOCUS AR049518
DEFINITION Sequence 5 fr
                                                                                                                                                                                       Unknown.
Unclassified.
                                                                                                                                                                         Unknown.
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                                 484 ysGln 485
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134 luTyrThrIleGluAlaTrpThrLysPheAspPheProGlyArgGlyAsn 150

401	::	450	
151	ThrHisSerAsnPheLysTrpArgTrpTyrHisPheAspGlyThrAspTr ::: :::	167 500	
167	PASPGINSETArgGInLeuGInAsnLySIIeTyrLySPheArgGIyThrG 	184	
184 551	1yıysalaTrpaspTrpGluValaspIleGluAsnGlyAsnTyrAspTyr 	200	
201	LeuwetTyralaAspIleAspWetAspHisProGluValIleAsnGluLe 	217 650	
217 651	uargasnītpglyValītpTyrThtAsnīhtLeuasnLeuaspGlyPhea ::	234	
234	rglleaspalavallysHisIleLysTyrSerTyrThrArgaspTrpLeu 	250	
251 751	ThrhisvalargasnThrThrGlyLysPrometPhealavalalagluPh 	267 800	
267	eTrpLysAsnaspLeuAlaAlalleGluAsnTyrLeuAsnLysThrSerT 	284 850	
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301 901	SerasnSerGlyGlyTyrPheaspMetArgasnIleLeuasnGlySerVa 	317 950	
317 951	1ValGlnLysHisProlleHisAlaValThrPheValAspAsnHisAspS 	334 1000	
334	erGlnProGlyGlualaLeuGluSerPheValGlnSerTrpPheLysPro 	350 1050	
351 051	LeualatyralaLeuileLeuthrargGluGlnGlytyrProservalPh 	367 1100	
367	eTyrGlyAspTyrTyrGlylleProThrHisGlyValbroSerMetLysS 	384 1150	
384	erlysileaspproleuleuGinalaargGinThrTyralaTyrGlyThr ::	400 1200	
401	GlnHisaspTyrPheaspHisHisaspIleIleGlyTrpThrargGluGl 	417 1250	
417	yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP :::::::::	434	
434	roGlyGlyAsnLysTrpMetTyrValGlyLysHisLysAlaGlyGlnVal :::	450	

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14-FEB-2001
                                                                                                                                                                                                                                                                           1 (bases 1 to 1455)
Bisg.ang.rd-Frantzen, H., Svendsen, A. and Borchert, T. Vedel.
Amylase variants
Patent: US 6093562-A 5 25-JUL-2000;
Location, Qualifiers
1. 1455
                    1301 CAGGGGGAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 ThrSerGlnAsnAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 yGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyThrArgSerG 84
                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 485
Gaps: 0
Percent Identity: 86.598
                                                                                                                                                                                              PAT
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                                                                                                                                                                                                       6093562
                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
473 a 227 c 352 g
                                                                                                                                                                               seq_documentation_block:
LOCUS AR104349 1455 bp DNA
DEFINITION Sequence 5 from patent US 6(
ACCESSION AR104349.1 GI:12817057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AR104349
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.148
Percent Similarity: 97.732
                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 2440.00
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US-09-590-375-2 x AR104349
                                                                                                                                                           seq_name: gb_pat:AR104349
                                                                                                                                                                                                                                                              Unknown.
Unclassified.
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Unknown.
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	AsnalaValGluValAsnArgSerAsnArgAsnGlnG 	134
134	luTyrThrIleGlualaTrpThrLysPheaspPheProGlyargGlyAsn ::	150 450
151	ThrhisserasnPheLysTrpargTrpTyrHisPheAspGlyThrAspTr ::: :::	167 500
167	PASPGInSerArgGlnLeuGlnAsnLysIleTyrLysPheArgGlyThrG 	184 550
184	1yLysalaTrpAspTrpGluValaspIleGluAsnGlyasnTyraspTyr 	200
201	LeuwetTyralaaspIleaspwetaspHisProGluVallleAsnGluLe 	217 650
217	uargasnītīpglyvalītīpīyrīhtrasnīhtreuasnīeuaspglyphea :::	234 700
234	rglleAspAlaValLysHisIleLysTyrSerTyrThrArgAspTrpLeu 	250 750
251	ThrHisValargasnThrThrGlyLysProMetPhealaValalaGluPh 	267 800
267	eTrplysasnaspleualaalailegluasnTyrLeuasnLysThrSerT TGGAAAATGATTTAGGTGCCTTGGAGAACTATTTAAATAAA	28 4 850
284	rpAsnHisSerValPheAspValProLeuHisTyrAsnLeuTyrAsnAla 	300
301	SerasnSerGlyGlyTyrPheAspMetArgAsnIleLeuasnGlySerVa 	317 950
317 951	ValGinlyshisproilehisalavalthrphevalaspasnhisaspS 	334 1000
334	erGlnProGlyGluAlaLeuGluSerPheValGlnSerTrpPheLysPro 	350 1050
351 1051	LeualatyralaLeulleLeuthrargGluGlnGlytyrProServalPh 	367 1100
367	eTyrGlyaspTyrTyrGly1leProThrHisGlyva1ProSerMetLysS 	384 1150
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401	GINHISASPTYrPheASPHISHISASPIleIleGlyTrpThrArgGluGl	417

	1.7.1 A 7.1	1451
	484 ysGln 485	484
1450		1401
484	467 pGlyTrpGlyAsnPheThrValAsnGlyGlyAlaValSerValTrpValL 484	467
1400		1351
467		451
1350	CAGGGGAGAGAATGGATGTACGTAGGCCAAAATAAAGCAGGTCAAGTT	1301
450		434
1300	. AAATACCACGCATCCCAATTCAGGACTTGCGACTATCATGTCGGGATGGGC 1300	1251
434	417 yAspSerSerHisProAsnSerGlyLeuAlaThrIleMetSerAspGlyP 434	417

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1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 60
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1: 405 Lexington Avenue
New York
New York
RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%; Score 2613; DB 2;
95.1%; Pred. No. 2.7e-223;
iive 16; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Nasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylasse
NUMBER OF SEQUENCES:
CARRESPONDENCE ADDRESS:
CARDESSEE: No. 58245310 No. 5824531disk of N
                       US-09-354-1918-7
US-09-264-097-6
US-09-264-097-8
US-08-264-099-6
US-08-343-804-6
US-08-343-804-6
US-08-687-399-6
US-08-683-8388-6
US-08-689-700-34
US-08-468-700-34
US-08-890-383-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
FILING DATE: U1-June-1995
CLASSIFICATION: 43
ATTORNEY/AGENT INFORMATION:
NAME: Harington, James J.
REGISTRATION NUMBER: 38,711
REPERENE/DOCKET NUMBER: 4157,204-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08446803
; Patent No. 5824531
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ottrup, Helle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.3'
Best Local Similarity 95.1'
Matches 461; Conservative
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STRANDEDNESS: sir
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US-08-446-803-1
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561.425 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-683-838A-12
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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SNSGGYFDMRNILNGSVVOKHPIHAVTFVDNHDSOPGEALESFVOSWFKPLAYALILTRE
                                         YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Wan Der Zee, Pia
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
CORRESPONDENCE: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Bisgard-Frant:
APPLICANT: Ostergaard, Pe
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PRIOR APPLICATION DATA:
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STATE: New York
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VWVKQ 485
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Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8;
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Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                    485 amino acids
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                                                                                                           STRANDEDNESS:
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US-08-600-908A-12
                                                                                                                                                                                US-08-861-837-1
                                                                    LENGIH:
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                                                                                         TYPE:
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No. 6022724th America, Inc.
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                                                                              ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 2613; DB 3;-
95.1%; Pred. No. 2.7e-223;
11ve 16; Mismatches 8;
 60227240 No. 6022724disk of
                  405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                       NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                  US/08/683,838A
                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/600,908
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                     United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
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Best Local Similarity 95.1:
Matches 461; Conservative
                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-867-01;
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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         STREET: 400 -
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                                                    STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.3%; Score 2613; DB 2; Best Local Similarity 95.1%; Pred. No. 2.7e-223; Matches 461; Conservative 16; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08683838A
Fatent No. 6023724
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: 'Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                         4394.204-US
                                 US/08/600,908A
                                                                 CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Green, Reze
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                13-FEB-1996
                                                                                                                                                                                                                                                  : 485 amino acids
amino acid
             CURRENT APPLICATION DATA
APPLICATION NUMBER: UFILING DATE: 13-FEB-1
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-600-908A-12
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481 VWVKQ 485
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SOFTWARE:
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RESULT 6
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                                                                                                                                         ADDRESSEE: No. 60935620 No. 6093562th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%; Score 2613; DB 3; Length 485; 95.1%; Pred. No. 2.7e-223; ive 16; Mismatches 8; Indels
                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Lamblinis, Ellas J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELECOMUNICATION INFORMATION:
TELEPHONE: 212 867 0228
TELEPHAX: 212 867 0298
                                                                                                    AMYLASE VARIANTS
                                                               APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
                                                                                                                                                                                                                                                                                 CUCRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
                          Sequence 1, Application US/08600656
Patent No. 6093562
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.19
Matches 461; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-600-656-1
                                                                                                                 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                                                                                                           SOFTWARE:
                                                             APPLICANT:
          US-08-600-656-1
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361 QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS 420
                           HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS 480
                                                                                                                         EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180
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95.1%; Pred. No. 2.7e-223;
iive 16; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-025
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1907-10-13
SAFFINER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFFWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 95.1%
Matches 461; Conservative
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                                                                Sequence 7, Application US/09170670
Patent No. 6187576
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgard-Frantzen Henrik
TILE OF INVENTION: Alpha-Amylase Mutants
FILE REPERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 95.1
Matches 461; Conservative
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                                                         US-09-170-670-7
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RESULT

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95.1%; Pred. No. 2.7e-223;
iive 16; Mismatches 8;
Sequence 1, Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Struiff, S ren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709,000-005
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 1
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APPLICANT: Svendsen, Allan
APPLICANT: Kyrulff, S ren
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase Variants
FILE REFERENCE: 5709,000-US
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Best Local Similarity 95.1
Matches 461; Conservative
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APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Blarne
APPLICANT: Nielsen, Blarne
APPLICANT: Niesen, Torben L.
APPLICANT: Kjaerulff, Soren
TITLE OF INVEWIION: Alpha-Amulase Mutants
FILE REFERENCE: 5369.200-030
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT PILING DATE: 1998-10-06
EARLIER RILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1990-11.
CURRENT APPLICATION NUMBER: US/09/193,068 CURRENT FILING DATE: 1998-11-16 NUMBER OF SEQ ID NOS: 31 SOFTWARE: FASTERO for Windows Version 3.0
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                                                                              TYPE: PRT ORGANISM: Bacillus sp. US-09-193-068-7
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96.3%; Score 2613; DB 4;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8;
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CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-07
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1997-10-30
EARLIER APPLICATION NUMBER: PA 1998 00936
EARLIER FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
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Patent No. 6204232
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Torben L.
APPLICANT: Nissen, Torben L.
APPLICANT: Kjærulff, Soren
TILE OF INVEWTION: Alpha-Amulase Mut
FILE REFERENCE: 5368.200-US
                                                                                                                                        TYPE: PRT
CORGANISM: Bacillus
US-09-183-412-1
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VWVKQ 485
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PatentIn Release #1.0, Version #1.25 (EPO)
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CITY: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   61 YDLYDLGEFNOKGTVRTKYGTRNOLQAAVTSLKNNGIQVYGDVVANNHKGGADGTEIVNAV 120
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                                                                                                                                                                                                                                                                                                                     EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE 360
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                                                                                                                                                     Length 485;
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                                                                                                                                                 Query Match
96.3%; Score 2613; DB 4;
Best Local Similarity 95.1%; Pred. No. 2.7e-223;
Matches 461; Conservative 16; Mismatches 8;
EARLIER TAPLICATION NUMBER: PA 1998 00936 SEARLIER FILING DATE: 1998-07-14 NUMBER OF SEQ ID NOS: 58 SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09354191A Patent No. 6297038 GENERAL INFORMATION:
                                                                                ; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-7
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                                                                    LENGTH: 485
                                                      SEQ ID NO 7
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241 IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
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95.1%; Pred. No. 2.7e-223;
tive 16; Mismatches 8;
                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 3728
REFERENCE/DOCKET NUMBER: 4318.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: No. 6287826man, Barrie Edmund APPLICANT: Hendriksen, Hanne Vang
         APPLICATION NUMBER: US/09/354,191A FILING DATE:
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/600,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/09264097; Patent No. 6287826
; GENERAL INFORMATION:
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
                                                                                                                                                                                                                                                                                   TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          LENGTH: 485 amino acids
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Best Local Similarity 95.13
Matches 461; Conservative
CURRENT APPLICATION DATA
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                   Length 485;
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup TITLE OF INVENTION: From Starch FILE REFERENCE: 5278.200-US CURRENT APPLICATION NUMBER: US/09/264,097
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08446803
| Patent No. 5824531
| GENERAL INFORMATION:
| APPLICANT: Ottrup, Helle
| APPLICANT: Ostrayand, Peter, Rabbek
| APPLICANT: Seamussen, Michael Dolberg
| TITLE OF INVENTION: Alkaline Bacillus Amylase
| TITLE OF INVENTION: Alkaline Bacillus Amylase
| CORRESPONDENCE ADDRESS:
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ص
                                                                                                                                                                                                                              96.2%; Score 2609; DB 4;
94.8%; Pred. No. 6.1e-223;
Live 16; Mismatches 9;
                                                CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER PILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 7
                                                                                                                                                                                                                           Query Match 96.2%
Best Local Similarity 94.8%
Matches 460; Conservative
                                                                                                                                                               TYPE: PRT
CORGANISM: Bacillus
US-09-264-097-7
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US-08-446-803-2
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                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLILOATION NUMBER: US/08/446,803
FILING DATE: 01-June-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2440; DB 2;
Pred. No. 5.6e-208;
40; Mismatches 25;
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
405 Lexington Avenue
                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.9%;
                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 2:
                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.68
Matches 420; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-446-803-2
                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                      New York
                   New York
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                                                       USA
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RESULT

No. 58245310 No. 5824531disk of No. 5824531th America

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                                                                                                                                                                                                                                                                                ZIP: 10174
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/861,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 2440; DB 2;
; Pred. No. 5.6e-208;
40; Mismatches 25;
                                                   APPLICANT: Ottrup, Helle
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
Sequence 2, Application US/08861837
Patent No. 5856164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
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86.6%;
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Best Local Similarity 86.6%
Matches 420; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                    GENERAL INFORMATION:
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starch-related polysaccharide; hydrolysis; enzyme; usrfactant resistance; alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent; dish-washing detergent; starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent;
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 Bacillus species KSM-AP1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-JP01641
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N-PSDB; AAT51339.
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(KAOS ) KAO CORP
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Bacillus strain NC
Termamyl-like alph
Wild type Termamyl
Bacillus parent Te
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1061.943 Million cell updates/sec
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Liquefied alkaline
Mutant alpha-amyla
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1 HHNGTNGTMMQYFEWHLPND.....ADGWGNFTVNGGAVSVWVKQ 485
                                                                                               Search time 33.83 Seconds
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             GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
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AAW31499
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AAY07391
AAY99602
                                                                   protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No.

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Alpha-amylase v Alpha-amylase v Alpha-amylase v

DNA encoding alkaline liquefying alpha-amylase - useful in dish-washing and laundry detergents for removal of starch dirts

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Alpha-amylase v Alpha-amylase v Alpha-amylase v

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                                        hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit resistance to surfactants used in detergents, and decompose starch or starch-related polysaccharides in a highly random manner. The Bacillus species KSM-AP1378, from which this sequence was isolated, is an alkalophilic Bacillus strain. It was isolated from soil in the vicinity of the city of Tochigi. The enzyme is detergents, particularly on starch dish-washing and laundry
                        This sequence represents an alkaline liquefying alpha-amylase.
Alpha-amylase is an enzyme that acts on starch-related polysaccharides,
                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                             271
                                                                                                                                                                                                                                                                                                                            IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
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                                                                                                                                                   Length 516;
                                                                                                                                                                   Indels
                                                                                                                                                100.0%; Score 2713; DB 18;
100.0%; Pred. No. 4.2e-219;
ive 0; Mismatches 0;
       Page 23-26; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW79904 standard; protein; 485 AA
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Best Local Similarity 100.
Matches 485; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VWVKQ 485
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                                                                                                                       Sequence
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        Claim
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The present sequence represents Bacillus licheniformis liquefied alkaline alpha-amylase. The present invention describes mutated forms of the liquefied alkaline alpha-amylase derived from Bacillus species KSM-AP1378 (FERM BP-3048), having the methionine residue at position 202 either deleted or substituted by another amino acid, such as threonine, asolucine, leucine, alanihe, valine or serine. The mutations (such as deletion of arginine or glycine at positions 181 and 182, respectively) but at least 95.2% homologous to positions 181 and 182, respectively) but at least 95.2% homologous to conditions, a high anylase activity, and a high and sustained conditions, a high anylase activity, and a high and sustained formulation of liquid, powder or granular detergent compositions, cespecially those containing bleaches and oxidants. The enzyme retains high activity in the presence of bleaches and oxidants allowing improved detergent formulations to be produced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                /note= "can be deleted or substituted by another acid residue such as Thr, Ile, Leu, Ala, or Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus derived alpha amylase having mutation at position 202 has optimum pH in alkaline conditions and high tolerance to oxidants, useful for production of detergent compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2704; DB 19;
Pred. No. 2.2e-218;
0; Mismatches 1;
Key Location/Qualifiers
Misc-difference 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.7%;
Best Local Similarity 99.8%;
Matches 484; Conservative
                                                                                                                                                                                                                                                                                                              97JP-0080299
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ikawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-542707/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 AA;
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                                                                                                                                                        WO9844126-A1
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                         SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
                                                                                                                                                                                         QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
                                                                                                                                                                                                          IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detergent compositions for hard surface cleaning and laundry use contains Bacillus derived alpha amylase with improved thermostability, reduced calcium ion dependency etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-amylase; hard surface cleaning; dishwashing; laundry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Pages 86-87; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  AAW31499 standard; protein; 485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohtani R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US03276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Ward G;
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512 vwvkg 516
                                                                                                                                                                                                                                                                                                    481 VWVKQ 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1997;
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Showell MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAW31499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a mutant alpha-amylase. Included in the invention are a gene encoding the mutant alpha-amylase, a vector containing the gene, and a transformed cell recombined by the vector. The enzyme is used in a detergent composition. The present sequence
420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180
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                                                                 QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
              HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Represented as Alu in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Represented as Aly in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A novel mutant alpha-amylase for use in a detergent composition
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Pred. No. 5.2e-218;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents the mutant alpha-amylase protein.
                                                                                                                                                                                                                                                                                    Mutant alpha-amylase amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                 Alpha-amylase; detergent; Bacillus
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                                                                                                                                                                                                       516
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99.6%;
                                                                                                                                                                                                    AAB35714 standard; protein;
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                                                                                                                                                                                                                                                            (first entry)
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                                                                                                         VWVKQ 485
                                                                                                                                   vwvkg 485
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                                                                                                                                                                                                                                                                                                                                          Bacillus sp
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485 AA;
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        Claim 1;
                                                        Sequence
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                                                                                                                                                                                                                    Alpha amylase; stain digestion; detergent; fabric laundry performance.
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                                                                                                                                                                 SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE 360
                                                                   ydlydlgefnqkgtvrtkygtrnqlqaavtslknngiqvygdvvmnhkggadgteivnav 120
              Gaps
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                                  YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV
                                                                                                                                                                      EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                           RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                                                                                                      IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA
                                                                                                                                                                                           QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
                           HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of specific alpha-amylase enzymes - in laundry detergent compositions to provide effective cleaning and whitening of dingy fabrics
              .;
0
 Length 485;
              Indels
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96.3%; Score 2613; DB 18;
95.1%; Pred. No. 9.3e-211;
tive 16; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                      alpha amylase protein #1
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              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-159168/14.
                                                                                                                                                                                                                                                                                             AAW48260 standard;
       Similarity
                                                                                                                                                                                                                                               VWVKQ 485
                                                                                                                                                                                                                                                            vwvkq 485
                                                                                                                                                                                                                                                                                                                                       sp.
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                                                                                                                                                                                                                                                                                                                                                               Bacillus sp
              461;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Baeck AC,
Showell MS;
Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                     Bacillus
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              Matches
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Alpha-amylase; cleaning composition; protease variant; spot removal; detergent composition; hard surface cleaning; fabric cleaning; dishwashing composition; oral cleaning composition; personal cleaning stain removal; soil removal; whiteness maintenance; dingy cleanup;
                                                                                                                                                                                                                                                                                                                                                                                              IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420
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be used
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                                                                                                                                                                                                                                                                                                                                   EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                                                                                                                                                                                                            HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                        Length 485;
                                        This sequence represents an alpha amylase from Bacillus sp. used in a laundry detergent. The detergent compositions can for boosting fabric laundry performance or for dingy fabric cleanup.
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                 Query Match 96.3%; Score 2613; DB 19; Best Local Similarity 95.1%; Pred. No. 9.3e-211; Matches 461; Conservative 16; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus sp. alpha-amylase protein fragment 1.
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Page 69-70; 82pp; English
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                                                                                                                                                                                                                        protease variant with an amino acid substitution corresponding to position 103 of Bacillus amyloliquefaciens and an alpha-amylase variant. The compositions can be used in e.g. detergent compositions, for cleaning compositions, or fabrics, dishwashing compositions, oral cleaning compositions, detergent cleaning compositions and personal cleaning compositions. The combination of protease variants and alpha-amylase variants in cleaning compositions can provide improved and enhanced cleaning ability, including stain and/or soil removal and/or reduction and/or whiteness maintenance and/or dingy cleanup and/or reduction film removal and/or reduction, over conventional enzyme-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 60
                                                                                                                                                                                                              invention describes novel cleaning compositions which contain a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                        Showell MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 2613; DB 20;
95.1%; Pred. No. 9.3e-211;
iive 16; Mismatches 8;
                                                                                                                                                                                    Claim 1b(ii); Page 164-165; 169pp; English
                                                                                                       Ohtani R,
                                                                                                       Ghosh CK,
                        97US-0956564.
97US-0956323.
97US-0956324.
 98WO-US22486
                                                                           (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                           New cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.11
Matches 461; Conservative
                                                                                                                                                                                                                                                                                                                                                            cleaning compositions
                                                                                                      Busch A,
                                                                                                                                WPI; 1999-404706/34
                                                                                                                                                                                                                                                                                                                                                                                     485 AA;
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                                     23-OCT-1997;
23-OCT-1997;
23-OCT-1998;
                          23-OCT-1997;
                                                                                                      Baeck AC,
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase: T141, K142, F143, D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, Q169, S170, R171, Q172, F173, P267, W268, K269, W270, D271, L272, G273, A274, L275, K311, G346, K385, G456, W457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present amylase can function as the parent sequence in the production of the variants of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVNRSNRNQE1SGEYT1EAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGTGKAWDWEVDI ENGNY DY LMY AD I DMDHPEV I NELRNWGVWYT NTLNLDGFRI DAVKH
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                                                                                                                                                                                                  Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process.
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                                                                                                                                                     Bacillus strain NCIB 12512 alpha-amylase protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Termamyl-like alpha-amylase variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 38; Page 77-79; 115pp; English.
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AAY15415 standard; protein; 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-DK00471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98DK-0000936,
97DK-0001240.
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                                                                                                   (first entry)
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Best Local Similarity 95.15
Matches 461; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-326987/27
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                                                                                                 22-JUL-1999
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                                                                                                                                                                                                                                                                                                      Bacillus sp.
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                                                 AAY15415;
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The specification describes termamyl-like alpha-amylase variants that have altered amino acid sequences to improve properties. The variants are produced by creating one or more of the following mutations in amino acid sequence of the parent termamyl-like alpha-amylase; T141, K142, F143, D144, F145, P146, G147, R148, G149, Q144, R181, G182, D183, G184, K185, A186, W189, S193, M195, H107, K108, G109, D166, W167, D168, Q169, S170, R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275, K311, E346, K365, G456, M457, K458, P459, G460, T461, V462, T463. The variants can be used for washing and/or dishwashing. They can also be used in the production of sweeteners and ethanol from starch, and/or for textile desizing, and in starch liquefaction and/or saccharification processes. The present amylase can function as the parent sequence in the production of the variants of the invention.
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                                                                                                                                           HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                                                                                                                                                        Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Termamyl-like alpha-amylase protein.
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97DK-0001240,
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Nissen TL,
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                                                                                                                          EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
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                                                                                                                                                                                                                                                        Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol.
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Misc-difference 181..184
/note= "optionally 1, 2, 3 or all residues are
Misc-difference 195
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except an Asn residue"
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Score 2613; DB 20;
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except a Glu residue"
                Pred. No. 9.3e; Mismatches
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      96.3%;
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      Query Match
Best Local Simi
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    useful as detergents

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                                      'optionally altered to except a Lys residue"
except a Glu residue"
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                                    "optionally
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                                                                                                                                                                                                                                                                                        Borchert TV,
                                                                                                                                                                                                                                                                                                                                                               Variant alpha-amylases - usefu
desizing or starch liquefaction
                                                                                                                                                                      98WO-DK00444.
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                                      /note=
                                                                                                                                                                                                                                                                                        Bisgard-Frantzen H,
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Matches 461; Conserv
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This sequence represents the parent sequence for new variants of a parent Termamyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol).
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    useful as detergents

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481 VWVKQ 485
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481 vwvkg 485
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                                                                                                                                                                                                                       AAY07391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a parent Termamyl-like alpha-amylase
from which mutants with increased stability at acidic pH, low calcium
concentration and high temperatures have been derived. The sequence
encoding this protein was isolated from a Bacillus genomic DNA library.
A variant may contain mutations in one or more solvent exposed amino
acid residues to increase the overall hydrophobicity of the enzyme or the
coverall number of methyl groups in the side chains of exposed residues
may be increased. The mutations can be incorporated by site-directed
mutagenesis or by random mutagenesis. As a result of their increased
stability, the variants are suitable for the industrial processing of
stability, the variants are suitable for the industrial processing of
starch, i.e. starch liquefaction and saccharification. They may also be
useful for washing, dishwashing and textile desizing. Hybrid
alpha-amylases comprising partial amino acid sequences derived from two
common and account of the company of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues
                                              300
                                                                                    360
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                                                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                      SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
                                                                                                QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
                                                                                                                                                                         HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ပ်
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus parent Termamyl-like alpha-amylase #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                       AAY99602
ID AAY99602 standard; Protein; 485 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme stability; hybrid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-387777/33.
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                                                                                                                         IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
                                                                                                                                                                                                                                                                                          HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS 480
                                                                                                                                                                                                                                                                                                                      QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS 420
                                                                                                                                                                                                                                                                                                                                  1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 60
                                                                                                                                                     EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
                                                                                                                                                                 RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                                                                                                                                                                         SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
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                                 Length 485;
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                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction; saccharification; mutein; mutant; enzyme stability; hybrid.
                              Score 2613; DB 21;
Pred. No. 9.3e-211;
; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kjaerulff S, Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus Termamyl-like alpha-amylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY99608 standard; Protein; 485 AA.
                                                  16;
                             96.3%;
95.1%;
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                                                   Conservative
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                                        Similarity
485 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        481 vwvkg 485
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                                                   461;
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Sequence
                             Query Match
Best Local S
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                                                Matches
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AW12098-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases represented by AWM12955, AAW12955, AAW12955 and AAR81835 and AAR81836.

AWM12098-W12136, AAW12141, AAW12142 and AWM12144 are specifically variants of the alkaphilic Bacillus strain NCIB 12512 alpha-amylase shown in AAR81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate. These variant alpha-amylolytic activity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in the production of sweeteners and
                                                                                   Alpha-amylase; detergent; thermal stability; oxidation stability; enzymcalcium ion. dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-amylase variants - with improved thermal and oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2611; DB 17;
Pred. No. 1.4e-210;
7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stability and reduced calcium ion dependency
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                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borchert T,
                                                                                                                                                                                                                                                                         /label= L217I
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94.8%;
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95DK-0000126.
                                               Alpha-amylase variant L217I.
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      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-371423/37
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                                                                                                                                                                                                                                                   Misc-difference 21
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      08-APR-1997
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29-MAR-1995;
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                                                                                                                                                                                          Synthetic.
                                                                                                                                               sweetener
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                                                                                                                                                            The present sequence is a parent alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence encoding this enzyme was isolated from a Bacillus genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are sultable for the industrial processing of starch, i.e. starch sultable for the industrial processing of starch, i.e. starch dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability.
                                        Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGTGKAWDWEVD I ENGNY DY LAYAD I DAMDHPEV I NELRNWGVWY TNTLNLDGFR I DAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.3%; Score 2613; DB 21;
95.1%; Pred. No. 9.3e-211;
Live 16; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW12113 standard; protein; 485 AA.
                                                                                                                         Claim 8; Page 62-64; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.11
Matches 461; Conservative
WPI; 2000-387777/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW12098-W12144 represent alpha-amylase variants of the invention. The variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding the parent alpha-amylases
                                                                                                                                        360
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evnrsnrngetsgeyaieawtkfdfpgrgnnhssfkwrwyhfdgtdwdgsrglgnkiykf 180
                       1KYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAA1ENYLNKTSWNHSVFDVPLHYNLYNA
                                                                             SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE
                                                                                                           QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
                RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svendsen A;
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                            AAW12129 standard; protein; 485 AA
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                                                                                                                                                                                                                                                                                                                                                              /label= E1900
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95DK-0000126.
95DK-0000336.
95DK-0001097.
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                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bisgard-frantzen H,
                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                       VWVKQ 485
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29-SEP-1995;
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                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                 sweetener
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represented by AAW12955, AAW12956, AAR81835 and AAR81836.

AAW1208-W12136, AAW12141, AAW12142 and AAW1214 are specifically variants of the alkaphilic Bacillus strain NCIB 12512 alpha-amylase shown in AAR81835.

These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylolytic activity (especially at pH values in the range of 8.5-10.5), and improved binding of a particular substrate.

These variant alpha-amylolytic activity (especially at pH values in the particular substrate, and/or improved specificity with respect to cleavage of substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants can also be used in the production of sweeteners and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.2%; Score 2610; DB 17; Length 485; 94.8%; Pred. No. 1.7e-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
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|| vwvkg: 485
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SNSGGYFDMRNILNGSVVQKHPIHAVTFVDNHDSQPGEALESFVQSWFKPLAYALILTRE

420 420 480

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421 HPNSGLATIMSDGPGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGGAVS
                                                                                                                 361 QGYPSVFYGDYYGIPTHGVPSMKSKIDPLLQARQTYAYGTQHDYFDHHDIIGWTREGDSS
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Crepresented by AAW12955, AAW12955, AAR81835 and AAR81836.

AAW12098-W12136, AAW12955, AAW12142 and AAW12144 are specifically variants of the alkaphilic Bacillus strain NCIB 12512 alpha-amylase shown on the ARR81835. These variants can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases also possess improved specificity to a charge variant alpha-amylases also possess improved specificity to a controllar substrate, and/or improved specificity with respect to cleavage of substrate, and/or improved specificity with respect to cleavage of substrate, and/or improved specificity with respect to cleavage of substrate, and/or improved specificity with respect to cleavage of substrate. These sequences can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase containts can also be used in papermaking and beer-making processes.
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94.8%; Pred. No. 1.7e-210;
Live 17; Mismatches 8;
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                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Bisgard-frantzen H, Borchert T,
                                                                                               /label= E1940
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95DK-0000126.
95DK-0000336.
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Matches 460; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ethanol from starch
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                                                                                Misc-difference
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29-MAR-1995;
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 sweetener
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181 181 241 IKYSYTRDWLTHVRNTTGKPMFAVAEFWKNDLAAIENYLNKTSWNHSVFDVPLHYNLYNA 300

EVNRSNRNQEISGEYTIEAWTKFDFPGRGNTHSNFKWRWYHFDGTDWDQSRQLQNKIYKF 180 RGTGKAWDWEVDIENGNYDYLMYADIDMDHPEVINELRNWGVWYTNTLNLDGFRIDAVKH 240

61 YDLYDLGEFNQKGTVRTKYGTRSQLQGAVTSLKNNGIQVYGDVVMNHKGGADGTEMVNAV 120

61 121

1 HHNGTNGTMMQYFEWHLPNDGNHWNRLRDDAANLKSKGITAVWIPPAWKGTSQNDVGYGA 60

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Search completed: November 28, 2001, 16:58:05
                            Job time: 208 sec
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Ratio: 4.327
Percent Similarity: 89.027
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-Q-Gqn2_1/USPTO_spool/US09590375/runat_28112001_152038_21070/app_query.fasta_1.1092
-DB-ISBUGd_PETENTS_NA -QFMT-fastap -SUFFIX-rn1 -GAPOP-12.000
-GABENT=4.000 -MINMATCH=0.100 -LOOPEXT-0.000 -LOOPEXT-0.000
-GGAPOP-4.500 -GGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-DELOP-6.000 -PGGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOP-6.000 -DELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-TRANS-human40.cdi -LIST=45 -DOCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST=0000000000
-TREADS-09590375_GCGN1_1.107 -NCPU-6 -ICDU-3 -LONGLOG
-USER-US09990375_GCGN1_1.107 -NCPU-6 -ICDU-3 -LONGLOG
-USER-UTMENOUT=120 -WARN_TIMEOUT=30 -NO_XLPXX -WAIT -THREADS=1
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/cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-468-700-33 + 1723.50 3236.08
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                                                                                 About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-09-590-375-1 to: Issued_Patents_NA:*
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ptodata/2/ina/6B_COMB.seq:US-
ptodata/2/ina/6B_COMB.seq:US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
Search tlme (sec): 64.100000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             : US-09-590-375-1
length: 480
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-468-220-31 + 1723.50 3236.08 ... /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-466-698-31 + 1723.50 3236.08 ... /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-704-706A-33 + 1723.50 3236.08 ... /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-890-383-1 + 1723.50 3236.08 ... /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-890-383-1 + 1723.50 3236.08 ... /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-914-679A-1 + 1723.50 3236.08 ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 66.460
                                                                                                                                                                                                                                                                                                                        APPLICANT: Ottrup, Helle
APPLICANT: Ottrup, Helle
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: No. 58245310 No. 5824531disk of STREET: 405 Lexington Avenue CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
TELEPA: (212) 878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      Sequence 5, Application US/08446803
Patent No. 5824531
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-590-375-1 x US-08-446-803-5
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157 CAAAATGATGTGGGGTATGGAGCCTATGATCTTTATGATTTAGGGGAATT 206 84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100 134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150 456 167 181 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197 198 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347 GlnalaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 207 TAATCAAAAGGGACGGTTCGTACTAAGTATGGGACACGTAGTCAATTGG ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 657 ATGGGGAGAATGGTATACAAATACATTAAATCTTGATGGATTTAGGATCG 231 spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 707 ATGCGGTGAAGCATATTAAATATAGCTTTACACGTGATTGGTTGACCCAT GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy |||||||| 757 GTAAGAAAGGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATTTTGGAA etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 29 51 257 101 307 357 134 407 151 167 507 182 214 314 1007 281 298 907 957 331

No. 58561640 No. 5856164disk of No. 5856164th America 1207 GATTATTTTGACCATCATAATATAATCGGATGGACACGTGAAGGAAATAC 1256 364 yaspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381 381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397 447 1407 GCCTAATTTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGAAACGA 1455 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480 431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr TyralaThr1leLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-5 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/861,837 . Alkaline Bacillus Amylase NAME: Harrington, James J.
REGISTATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 5: FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-JUNE-1995
ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS STREET: 405 Lexington Avenue CITY: New York SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: New York : USA 10174 ADDRESSEE: COUNTRY: STATE: 348 1257 464 398 448

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TGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA
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|57 CATGGGATTGGGAAGTAGATTGGAAATGGAAATTGATTAATG
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                                                                                                                                       Length: 483
Gaps: 2
Percent Identity: 66.460
                                                                                                                                                                                                                                                 to: 1455
                                                                                                                                                                                                                                                 from: 1
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                                                                                                                                                                                                  alignment_block:
US-09-590-375-1 x US-08-861-837-5
           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
LENGTH: 1455 base pairs
                                                                                                                                     Ouality: 1860.50
Ratio: 4.327
Percent Similarity: 89.027
                                                                                                                          alignment_scores:
                                                                         us-08-861-837-5
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spAlalleLysHislleProPheTrpTyrThrSerAspTrpValArgHis
                                          etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
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                                                                                                                                              GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
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APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
; Sequence 5, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
                                                                                                                                              248
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E: No. 60935620 No. 6093562disk of No. 6093562th America, Inc. 405 Lexington Avenue, Suite 6400
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                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 2
Percent Identity: 66.460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                               4318.204-US
                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 4318.204-US
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-590-375-1 x US-08-600-656-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1455 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.327
Percent Similarity: 89.027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 1860.50
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                      New York
          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                     STREET: 4
CITY: New
STATE: Ne
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yaspTyrTyrGlylleProAsnAspAsnIleSerAlaLysLysAspMetI 381
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                   hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
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1307 GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
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Percent Identity: 66.460
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APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
APPLICANT: Bisgard-Frantzen Henrik
TTLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276 200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-18
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
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Ratio: 4.327
Percent Similarity: 89.027
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US-09-170-670-10
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LENGTH: 1455
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206 1207 GATTATTTGACCATCATATATATCGGATGGACACGTGAAGGAAATAC 1256 431 lySerLySTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447 448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464 29 1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-15 Length: 483 Gaps: 2 Percent Identity: 66.460 to: 1455 seq_documentation_block:
Sequence 15, Application US/09170670
Patent No. 6187576
GERRAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
TITLE NO INVENTION: Alpha-Amylase Mutants
FITLE REFERENCE: 5276, 200-US
CURRENT FILING DATE: 1998-110-13
EARLIER PELLING DATE: 1997-10-13
EARLIER PELLING DATE: 1997-10-13
EARLIER PELLING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
SERVITH: 1455 Align seg 1/1 to: US-09-170-670-15 from: 1 $us-09-590-375-1 \times us-09-170-670-15$ Quality: 1860.50 Ratio: 4.327 nilarity: 89.027 ; TYPE: DNA ; ORGANISM: Bacillus sp. US-09-170-670-15 Percent Similarity: alignment_scores: alignment_block: 157 107 51

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1307 GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
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                                                                  398 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
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Identity: 66.460
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APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Andersen, Carsten
TITLE OF INVENTION: -Amylase variants
FILE REFERENCE: 5709 .000-02
CURRENT APPLICATION NUMBER: US/09/193,068
CURRENT FILING DATE: 1998-11-16
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 1455
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Sequence 10. Application US/09193068
Patent No. 6197565
GENERAL INFORMATION:
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US-09-590-375-1 x US-09-193-068-10
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Percent Similarity: 89.027
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US-09-193-068-10
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Percent Identity:
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    Sequence 14, Application US/09193068
    Patent No. 6197565
    GENERAL INFORMATION:
    APPLICANT: Strondsen, Allan
    APPLICANT: Strulff, S ren
    APPLICANT: Bisgaard-Frantzen, Henrik
    APPLICANT: Andersen, Carsten
    TITLE NOF INVENTION: -Amylase Variants
    FILE REFERENCE: 5709.000-US
    CURRENT APPLICATION NUMBER: US/09/193,068
    CURRENT APPLICATION NUMBER: US/09/193,068
    CURRENT FILING DATE: 1998-11-16
    NUMBER OF SEQ ID NOS: 31
    SEQ ID NO 14
    LENGTH: 1455
    TUPE: Num
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Percent Similarity: 89.027
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US-09-193-068-14
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GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67

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SECTION SECTIO
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. AAAGCATCCAATGCATGCCGTAACTTTTGTGGATAATCACGATTCTCAAC
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AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs

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1057 TATGCGCTTATTTTAACAAGAGAACAAGGCTATCCCTCTGTCTTCTATGG 1106
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                                                                                                                                                                                                                                                                                              414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG
                                          yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                                                                                            381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Mielsen, Earten
APPLICANT: Mielsen, Bjarne
APPLICANT: Missen, Torben L.
APPLICANT: Missen, Torben L.
APPLICANT: Missen, Torben L.
TITLE OF INVENTION: Alpha-Amulase Mutants
FILE REFERENCE: 5368,200-US
CURRENT APPLICATION NUMBER: US/09/183,412
CURRENT APPLICATION NUMBER: 60/064,662
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1998-10-17
EARLIER FILING DATE: 1998-07-17
EARLIER FILING DATE: 1998-07-17
EARLIER PILING DATE: 1998-07-14
EARLIER FILING DATE: 1998-07-14
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
    Sequence 10, Application US/09183412
    Patent No. 6204232
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-183-412-10
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                                   nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 34
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                                                                                                                                    GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-183-412-14

pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480

464

PACENT NO. 0.204232

PATCHIN NO. 0.204232

APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Svendsen, Allan
APPLICANT: Nalesen, Carsten
APPLICANT: Nielsen, Bjarne
APPLICANT: Nielsen, Bjarne
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, Torben L.
APPLICANT: Nissen, 1200-18

CURRENT APPLICATION NUMBER: 06/064,662
EARLIER APPLICATION NUMBER: 60/093,234
EARLIER FILING DATE: 1998-10-17

EARLIER FILING DATE: 1998-07-17

EARLIER FILING DATE: 1998-07-17

EARLIER FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 58

NUMBER OF SEQ ID NOS: 58

SEQ ID NO 14 9_documentation_block: Sequence 14, Application US/09183412 Patent No. 6204232 TYPE: DNA ORGANISM: Bacillus

207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGGACACGTAGTCAATTGG 256 84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100 hrileAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197 ||||||||:::|||:::|||:::|
ATGGGGAGAATGGTATACAATACATTAAAATCTTGATGATTTAGGATCG 706 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134 557 CATGGGATTGGGAAGTAGATTCGGAAAATGGAAATTATGATTATTAATG 606 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214 PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA 231 spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247 17 26 67 84 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 34 34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG TCAGACTTTAAATGGCGTTGGTATCATTTCGATGGTGTAGATTGGGATCA 607 TATGCAGATGTAGATATGGATCATCCGGAGGTAGTAAATGAGCTTAGAAG 1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs Percent Identity: 66.460 to: 1455 from: 1 Align seg 1/1 to: US-09-183-412-14 alignment_block: US-09-590-375-1 x US-09-183-412-14 Quality: 1860.50 Ratio: 4.327 Percent Similarity: 89.027 alignment_scores: 17 51 67 257 101 307 117 357 134 407 151 457 167 507 182 198 214 657 231 707

298

314

331

348

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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 TGATGGGAATCACTGGAATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 GTAGTGAACCATAAAGGAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC
                                                                                                          PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 TGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spalaGlyIleThralaIleTrpIleProProAlaTyrLysGlyAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 483
Gaps: 2
Percent Identity: 66.460
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                                                                                                                                                                                                                                                                                                                                                 4318.204-US
                                  MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMITN Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,191P
                                                                                                                                                   US/09/354,191A
                                                                                                                                                                       CLASSIFCCATION:
CLASSIFCCATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/600,656
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Ellas J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.2C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0123
TELEPHONE: 212 867 0298
: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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US-09-590-375-1 x US-09-354-191A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouality: 1860.50
Ratio: 4.327
Percent Similarity: 89.027
                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-354-191A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: No. 62970380 No. 6297038th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007 CTGGGGGAATCATTAGAATCATTTGTACAAGAATGGTTTAAGCCACTTGCT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              957 AAAGCATCCAATGCCATGCCGTAACTTTGTGGGATAATCACGATTCTCAAC 1006
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                                                                                   264 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281
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                                        757 GTAAGAAACGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATTTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
                                                                                                          281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
                                                                                                                                                                                                248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
                                                                                                                                                                                                                                                           GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
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APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New York
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1307 GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356

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167 nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
                                                                                                                                                       GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214
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                                                                                                                                                                                                                                                                                                             331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
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                                                                                                                                                                                                                                                           SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl
                                                                                                               ATCACGACAATTCCAAAATCGTATCTACAAATTCCGAGGTGATGGTAAGG
                                                                                                                                         . TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu
                                                                                                                                                                                                                                            PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA
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E\colon No. 5824531o No. 5824531disk of No. 5824531th America 405 Lexington Avenue
                          AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-446-803-4
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Percent Identity: 66.253
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,803
FILING DATE: U1-June-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ottrup, Helle
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rabbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               Sequence 4, Application US/08446803
Patent No. 5824531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-446-803-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-590-375-1 x US-08-446-803-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouality: 1835.50
Ratio: 4.319
Percent Similarity: 87.992
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COMPUTER READABLE FORM:
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STRANDEDNESS: sing
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448
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756
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                                                                                                                     84
              GlnalaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh
                                                                                                                    eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
                                                                                                                                                TAACCAGAAGGGGACGGTTCGTACAAATATGGAACACGCAACCAGCTAC
                                                                                                                                                                                             607 TATGCAGACGTGGATATGGATCACCCAGAAGTAATACATGAACTTAGAAA
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                                                                                      CAGAATGATGTAGGTTATGGAGCCTATGATTTATATGATCTTGGAGAGTT
                                                                                                                                                                                                                                                                    GTCGTCATGAATCATAAAGGTGGAGCAGATGGTACGGAAATTGTAAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
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spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer
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ADDRESSEE: No. 58561640 No. 5856164disk of No. 5856164th America STREET: 405 Lexington Avenue CITY: New York STATE: New York 1357 GATATTACCGGAAATAGGACAGCACCGTCACAATTAATGCAGACGGATG 1406 1307 GTAACAAATGGATGTATGTGGGGAAAAATAAAGCGGGACAAGTTTGGAGA 1356 431 lySerLySTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-861-837-4 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Ostergaard, Peter Rahbek
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Van Der Zee, Pia
TITLE OF INVENTION: Alkaline Bacillus Amylase
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS: REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 4157.204-US
TELECOMMUNICATION INFORMATION: GENERAL INFORMATION:
APPLICANT: Ottrup, Helle
APPLICANT: Bisgard-Frantzen, Henrik PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,803
FILING DATE: 01-June-1995
ATTORNEY/AGENT INFORMATION: US/08/861,837 seq_documentation_block:
; Sequence 4, Application US/08861837
; Patent No. 5856164 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible Harrington, James J. CURRENT APPLICATION DATA: APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435 USA ZIP: 10174 COUNTRY: 364 448 1001 1057 1107 331

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607 TATGCAGACGTGGATATGGATCACCCCAGAAGTAATACATGAACTTAGAAA 656
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                                                                                                                                                                                                                                                   Percent Identity: 66.253
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                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TELEPHONE: (212) 867-0123
TELEFAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1455 base pairs
                                                                                                                                                                                                                                     Ratio: 4.319
Percent Similarity: 87.992
                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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Ratio: 4.319
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                                            spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
                                                                                           248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
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aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134

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                                                                        ADDRESSEE: No. 60935620 No. 6093562disk of No. 6093562th America, Inc. STREET: 405 Lexington Avenue, Suite 6400
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                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,656
FILLING DATE: 13-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 TAACCAGAAGGGGACGGTTCGTACAAATATGGAACACGCAACCAGCTAC
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Percent Identity: 66.253
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CLASSIFICATION NUMBER:

CLASSIFICATION:

A 43 CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4318.204-US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPRAX: 212 867 0123

TELEFRAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 4:
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-600-656-4
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US-09-590-375-1 x US-08-600-656-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
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LENGTH: 1455 base pairs
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Ratio: 4.319
hilarity: 87.992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                          STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
                                                                                                             New York
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uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP
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AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
                                                                                                                                                        pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-170-670-9
                                                                                                                                                                                                                                  eq_documentation_block:
Sequence 9, Application US/09170670
Patent No. 6187576
                                                                                                      448
                                                                                                                                                        464
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GREERAL INCORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants;
FILE REFERENCE: 5276-200-02
CURRENT APPLICATION NUMBER: US/9/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-3
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1455 ; TYPE: DNA ; ORGANISM: Bacillus sp. US-09-170-670-9

Gaps: 2 Percent Identity: 66.253 Length: alignment_block: US-09-590-375-1 x US-09-170-670-9 Ratio: 4.319 Percent Similarity: 87.992 Quality: 1835.50 alignment_scores

Align seg 1/1 to: US-09-170-670-9 from: 1 to: 1455

20 34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

6	leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGl	00
381	yaspTyrTyrGlyIleProasnaspAsnIleS GATTACTACGTATCCCAACCCATGGTGTTO	364
364	TyralathrileLeuthrargGluGlyGlyTyrPr ::: TATGCATTGGTTCTGAAGGGAACAAGGTTATCC	348
347	roGlyGluSerLeuGluSerTrpValAla CGGGGAAGCATTGGAATCCTTTGTTCAA	331
331	4 ualaHisPrometHisAlaValThrPheValAspAsnHisAspThrGlnP:::	314
314	GlnGlyGly ::: AGCGGTGGT	298
297	. etSerLeupheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln ::: ::: ::: ACTCGGTGTTTGATGTTCCTCTCCACTATAATTTGTACAATGCATCTAAT	281
281	sAspAspValG1yAlaLe ::: ::: AAATGACCTTGGTGCAAT	264
264	GlnargasnGlualaaspGlna GTGCGTAACACCACAGGTAAAC	248
247	spalalleLysHislleProPheTrpTyrThrSeraspTrpValargHis	233
231	rTrpPheThraspGl ::: ::: GTGGTATACGAATAC	214
214	AspPheSerHisProGluValGlnA :::::: GATATGGATCACCCAGAAGTAATAC	198
197	2TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu ::: :::	183
18: 55(rGlnGluAsnHi. ::: GCTTCAAACAA	167
167	1 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 	15.
15(45(4 hrileaspalatrpThrGlyPheaspPheserGlyArgasnAsnAlaTyr :: ::	134
134	7 avalGlnvalAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT ::: ::: : GGTAGAAGTGAATCGAACCGAAACCAGGAAACTCAGGAGAGTATG	357
356	1 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 	30.
306	:: :::	25.

eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG

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GTAACAAATGGATGTATGTGGGGAAAAATAAAGCGGGACAAGTTTGGAGA 1356
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                                                                                                                                                              431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr
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Percent Identity:
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APPLICANT: Svendison, Allan
APPLICANT: Borchert, Torben
APPLICANT: Borchert, Torben
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5276.200-US
CURRENT APPLICATION NUMBER: US/09/170,670
CURRENT FILING DATE: 1998-10-13
EARLIER APPLICATION NUMBER: 1172/97
EARLIER FILING DATE: 1997-10-13
EARLIER FILING DATE: 1997-10-28
NUMBER OF SEC ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                             eq_documentation_block:
Sequence 14, Application US/09170670
Patent No. 6187576
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US-09-590-375-1 x US-09-170-670-14
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Ratio: 4.319
nilarity: 87.992
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SECTIVE SECTION SECTIO
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364 yAspTyrTyrGlylleProAsnAspAsnIleSerAlaLysLysAspMetI 381		
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1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
                                                                                                                                                                                                                                                                                                                                       Sequence 1745 BP; 509 A; 283
                                                   AAA70314 standard; DNA; 1745
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98JP-0362488.
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Ratio: 5.598
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Percent Similarity: 100.000
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                                                                                                                                                                                                                       Kitayama
                                                                                                                                                                                                                                 WPI; 2000-516014/47
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                                                                                                                                                                                                            (KAOS ) KAO CORP
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                                                                                                                                                         EP1022334-A2
                                                                                                                                                                                20-DEC-1999;
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                                                                          19-DEC-2000
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                                                                                                                Bacillus sp.
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                                                               AAA70314;
                                                                                                                            Key
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3.8e-153
2.8e-153
3.8e-153
5.6e-153
7.0e-153
7.0e-153
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7.1e-153
7.1e-153
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8e-165
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5e-163
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                           Copyright (c) 1993-2000 Compugen Ltd
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No
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7.3e-153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp. The invention concerns the isolation of two new liquefying alpha-amylases (and their coding sequences) from Bacillus sp. strains KSM-K36 and KSM-K36, designated K36 and K38, of which this sequence encodes one. The alpha-amylases of the invention are chelating-agent resistant and thus are useful in the starch, brewing, fibre, pharmaceutical and food industries, and especially as components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liquefying alpha-amylase; detergent; starch industry; brewing industry; pharmaceutical industry; food industry; fibre industry; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful in a detergent composition not less than 70 % when treated under
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/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV09764 + 1723.50
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                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA70314
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Gaps: 0
Percent Identity: 100.000
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190..1695
/*tag= a
/product= "alpha-amylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 24-27; 34pp; English.
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Liquefying alpha-amylase; detergent; starch industry; brewing industry; pharmaceutical industry; food industry; fibre industry; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA70313
317 oMetHisAlaValThrPheValAspAsnHisAspThrGlnProGlyGluS
                                                                                                                                                                                              erLeuGluSerTrpValAlaAspTrpPheLysProLeuAlaTyrAlaThr
                                                                                               351 IleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGlyAspTyrTy
                                                                                                            rGlyIleProAsnAspAsnIleSerAlaLysLysAspMetIleAspGluL
                                                                                                                                                                                                                                              AspHisTrpAspValValGlyTrpThrArgGluGlySerSerArgPr
                                                                                                                                                                                                                                                            OASnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyGlySerLysT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
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/product= "alpha-amylase"
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65..1570
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98JP-0362488.
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ID AAA70313 standard;
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21-DEC-1998,
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1378 TAATTCGGGTCTTGCTATTATGTCCAATGGTCCTGGAGGATCAAAAT
                                                              rpargValAspGluGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsn
                                                                                                                                                                                          rTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleL
                                                                                                                                                                                                          ysHisIleProPheTrpTyrThrSerAspTrpValArgHisGlnArgAsn
                                                                                                                                                                                                                                                                                                                                 heAspValProLeuAsnTyrAsnPheTyrArgAlaSerGlnGlnGlyGly
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   nArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnT
                GGCGAGTGGATGAATGGTAATTATGACTATTATTAGGATCGAAC
                                                                                                                            11eAspPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySe
                                                                                                                                                                                                                                                                   GluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLysAspAspVa
                                                                                                                                                                                                                                                                                                                                                                             1GlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluMetSerLeuP
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                                                                                                                                                                        The present sequence is the coding sequence of a novel alpha-amylase from Bacillus sp. The invention concerns the isolation of two new liquefying alpha-amylases (and their coding sequences) from Bacillus sp. strains KSW-K36 and KSW-K38, designated K36 and K38, of which this sequence encodes one. The alpha-amylases of the invention are chelating-agent resistant and thus are useful in the starch, brewing, fibre, pharmaceutical and food industries, and especially as components of
                                                                            useful in a detergent composition not less than 70 % when treated under
   χ.
   Ozaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ATGCGGGTATTACAGCTATTTGGATACCCCCAGCCTACAAAGGAAATAGT
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                                                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                                                                                                            Length: 480
Gaps: 0
Percent Identity: 96.458
 ×
Igarashi
                                                                                                                                                                                                                                                                                                                 C; 420 G; 488 T;
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 Hayashi Y,
                                                                                                                                          Claim 6; Page 20-23; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                            New liquefying alkaline amylase, comprises a residual activity of
                                                                                                                                                                                                                                                                                                                   267
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5.477
99.583
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 Kitayama
                             WPI; 2000-516014/47
P-PSDB; AAB14821.
                                                                                                           specific conditions
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 Hagihara H,
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467 ePheThrAsnGlyGlySerValSerValTyrValAsnGln 480

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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from 2C Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311) and have improved wash performance in alkaline detergent solutions (pH 9-11) and have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 6.0. The invention also relates to mutants (AAB2918-B2934) of the covel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally convel alpha-amylases active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs are useful in a detergent composition of these narymaes are useful for etchanol production. In particular, the pulp and paper industry, for brewing or baking, or as laundry, especially useful for removing starch possitions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for convenient of the sequence represents DNA encoding a novel Bacillus mature alha-amylases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-amylase; AAI-6; AAI-10; DSW 12650; DSW 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nielsen VS;
                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA97708
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus sp. mature alpha-amylase DNA, SEQ ID NO:1.
1528 CITTACAAATGGAGGATCTGTATCCGTGTATGTGAACCAA 1567
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Svendsen A, Andersen C;
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ID AAA97708 standard; DNA; 1458
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99DK-0000489
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13-APR-1999;
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Quality: 1910.50

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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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                                                                                                                                                                    17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA
                                                                                                                                                                                                                          34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer
                                                                                                                                                                                                                                                                                                                                          eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl
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  Gaps: 2
Percent Identity: 68.944
                                                                                     to: 1458
                                                                                   from: 1
4.412
89.648
                                                                                  to: AAA97708
                                     alignment_block:
US-09-590-375-1 x AAA97708
          Percent Similarity:
                                                                                  Align seg 1/1
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Borchert TV, Nielsen VS;

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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and noted a control of a c
                                                                                                                                                                                                                                                                                                                                  New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
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Gaps: 2
Percent Identity: 68.944
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                                                                                                                                                                                 Nielsen BR,
  28-MAR-2000; 2000WO-DK00147
                                                   99DK-0000438
99DK-0000489
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  Alpha-amylase; AAI-6; AAI-10; DSW 12650; DSW 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1057 TATGCAACGATTCTTACGAGAGAACAAGGCTACCCACAAGTGTTTACGG 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATTATTATGGTATTCCGAGTGATGGCGTTCCAAGCTATCGTCAACAAA 1156
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AGCGGCGGAAATTACGACATGAGAAATTTGTTAAATGGAACGCTCGTTCA 956
                                                                                                                                                                                                                                                                                       314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
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                                                                                                      414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG
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                                                                              etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
                                                                                                                                                                              298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
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ID AAA97709 standard; DNA; 1458
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eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG 84

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09-FEB-2001

AAA97709;

Bacillus sp

12-OCT-2000

84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100 134 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150 101 ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117 264 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln 297 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134 182 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281 PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn.... 607 TATGCAGACGTTGACATGGATCAGCAGGAGTGATTAACGAACTAAACCG roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 407 AAATCGAAGCATGGACAGGGTTCAATTTTCCTGGACGTGGCAATCAACAT SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl spAlaIleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 507 857 957 348 1057 117 151 167 198 214 657 231 707 248 757 264 281 1007 807 331

This DNA sequence may be expressed recombinantly for the production of an alpha-amylase protein. The produced protein is characterized by having a specific activity at least 25% higher than the specific activity of Termamyl at 25-55 deg C and a pH of 8-10. The enzyme can be used in detergent composition for starch liquefaction, the production of lignocellulosic materials, e.g. pulp, paper and cardboard from waste containing starch, for deinking recycled starch-coated, or starch- containing printed paper, to modify compsns. starch liquefaction, textile desizing, starch modification or beer making Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile; Rasmussen MD; CGATTATTATGGCATCCCAAGTGACGGTGTTCCAAGCTACCGTCAACAGA 1156 1157 TCGACCCACTTTTAAAAGCTCGTCAACAATATGCTTATGGTAGACAGCAC 1206 464 431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447 seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA1995.DAT:AAT00777 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr Outtrup H, Bacillus sp. alkaline alpha-amylase DNA. Ostergaard PR, Disclosure; Page 50; 65pp; English. 95DK-0000123. AAT00777 standard; DNA; 1455 94DK-0000353. 94DK-0001271. 95WO-DK00142 16-MAR-1996 (first entry) (NOVO) NOVO-NORDISK AS Bisgard-frantzen H, WPI; 1995-351318/45. seq_documentation_block: beer; starch; ss. Van DER ZEE P; WO9526397-A1 29-MAR-1995; 03-FEB-1995; 29-MAR-1994; 03-NOV-1994; 05-0CT-1995 AAT00777; Bacillus. 398 448 381 414

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                                                                                                                                                                                                                                                                                                       GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 67
                                                                                                                                                                       84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGGATTGGGAAGTAGATTCGGAAAATGGAAATTATGATTATTAATG
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                                                                                                                                                                                                                                                                                                                                                             hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
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                               other;
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Gaps: 2
Percent Identity: 66.667
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nilarity: 89.027
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Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
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                                                                                                                                                                                                                    rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG
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                                                                                                    GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
                                GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
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ID AAX59633 standard; DNA; 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes termamyl-like alpha-amylase variants that
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Percent Identity: 66.460
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97DK-0001240
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Percent Similarity: 89.027
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US-09-590-375-1 x AAX59633
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                                                    WO9923211-A1
                                                                                                                               30-OCT-1998;
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30-OCT-1997;
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                                                                                           14-MAY-1999
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207

eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG

Align seg 1/1

34

51

157 29

84

84 luArgAlaileGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100

= = =

leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis 397 |||||| :::|||:::|||||||||||| TTGATCCAATCTTAGGAACACAACAT 1206 AAAGCATCCAATGCATGCCGTAACTTTTGTGGATAATCACGATTCTCAAC 1006 1107 TGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAGCCAAGA 1156 181 556 ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197 909 607 TATGCAGATGTAGATATGGATCATCAGGAGGTAGTAAATGAGCTTAGAAG 656 231 314 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347 364 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150 SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 214 231 spAlalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis 247 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264 SASpAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281 297 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331 yAspTyrTyrGlylleProAsnAspAsnIleSerAlaLysLysAspMetI 381 GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 557 CATGGGATTGGGAAGTAGATTCGGAAAATGGAAATTATGATTATTAATG PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 364 381 1157

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Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Termamyl-like; alpha-amylase; variant; washing; dishwashing; production; sweetener; ethanol; starch; textile desizing; starch liquefaction; saccharification process; ss.
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                 ASPTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
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ID AAX59637 standard; DNA; 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 CATGGGATTGGGAAGTAGATTCGGAAAATGGAAATTATGATTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGGGAGAATGGTATACAATACATTAAATCTTGATGGATTTAGGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
Length: 483
Gaps: 2
Percent Identity: 66.460
                                                                                                                     to: 1455
                                                                                                                   from: 1
                                                                                                                 Align seg 1/1 to: AAX59637
                 Ratio: 4.327
Percent Similarity: 89.027
 Quality: 1860.50
                                                                alignment_block:
US-09-590-375-1 x AAX59637
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Variant; Termamyl; alpha-amylase; mutation; Bacilius; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wild type Termamyl(RTM)-like alpha-amylase coding sequence #2.
                                                                                                                                                                                                                                                                                                   1056
                                                                                                                                                                                                                                                                                                                                                                                                                                            364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381
                                                                                                                                                                                                                                 314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1407 GGCTAATTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGAAACGA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57593
                                                                                                                                                                                                                                                                                                                                                  757 GTAAGAAACGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATTTTTGGAA
                                                                     sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM
                                                                                     281 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
                                                                                                                                                         298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
                                                                                                                                                                                                                                                                                                                                                                                                                      348 TyralaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
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ID AAX57593 standard; DNA; 1455
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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamyl-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. myloliquefactions or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol).
                                                                                                                                                                                                             for textile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AATGGGACAAATGGGACGATGATGCATATGAATGGCACTTGCCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 483
Gaps: 2
Percent Identity: 66.460
                                                                                                                                                                                                             or
                                                                                                                                                                                                           detergents
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                                                                                                                                                                                                                                                 Disclosure; Page 77-78; 93pp; English.
                                                                                                                                                                                                          - useful as
                                                                                                                                                 Borchert TV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
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desizing or starch liquefaction
                                                                                     97DK-0001172
                                                           98WO-DK00444
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                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1860.50
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Percent Similarity: 89.027
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                                                                                                                                               Bisgard-Frantzen H,
                                                                                                                                                                            WPI; 1999-277632/23
WO9919467-A1
                                                                                       13-OCT-1997;
                                                          13-OCT-1998;
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                                                                                                                                         607 TATGCAGATGTAGATATGGATCATCCGGAGGTAGTAAATGAGCTTAGAAG
                                                                                                                                                                                                                                                                                                                                               leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
          214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA
                                                                                                                                                                                                                               spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
                                                                                                                                                                                                                                                                          uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1057 TATGCGCTTATTTTAACAAGAGAACAAGGCTATCCCTCTGTCTTCTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAGCCAAGA
hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
                                                                                    nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn....
                                                                                                                                                                         GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs
                                                                                                                                                                                                                                                                                                       GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
                                                                                                                                                                                                                                                                                                                          757 GTAAGAAACGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATTTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                    298 GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
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                                          SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl
                                                                                                                               ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu
                    407
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134
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This sequence represents the coding sequence for a parent sequence used to generate new variants of a Termamy!-like alpha-amylase with alpha-amylase activity. The variants comprise mutations in 2-6 regions/positions relative to an alpha-amylase from either of two Bacillus species in W09526397, B. stearothermophilus, B. licheniformis, B. amyloliquefactions or Bacillus sp. #707. The alpha-amylase variants are detergent additives for use in detergents for dishwashing, manual or automatic laundry. The variants can also be used for textile desizing or starch liquefaction (e.g. for production of sweeteners or ethanol).
                                                                                                                                                                                                                                                                                                                                                 Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent; dishwashing; laundry; textile; desizing; starch liquefaction; sweetener; ethanol; ss.
                                                                                                                                                                                                                                                                                                                     Wild type Termamyl(RTM)-like alpha-amylase coding sequence #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for textile
pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX57598
                                                           448 AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr
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2
66.460
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    useful as detergents

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Percent Identity:
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                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        desizing or starch liquefaction
                                                                                                                                                                                                              seq_documentation_block:
ID AAX57598 standard; DNA; 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-DK00444.
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                                                                                                                                                                                                                                                                                          (first entry)
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Ratio: 4.327
Milarity: 89.027
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9919467-A1
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Thu Nov

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hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
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                                                                                                                         67
                                                                                                                                                                         84
7 AATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCCTAA 56
                                                                                                                         GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh
                                                                                                                                                                       eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
                                                                                                                                                                                       207 TAATCAAAAGGGGACGGTTCGTACTAAGTATGGGACACGTAGTCAATTGG
                                                                                                                                                                                                                                                                                                                                                                                   214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA
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1307 GAGAGAAATGGATGTACGTAGGCCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
                                                                                                                                                  yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
                                                                                                                                                                                                                                                                                                                                                   431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpfhr 447
                                                                                                                                                                                                                                                                                                                                                                                                      AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
  331
                                                                                                                                                                                                                                                   AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1407 GGCTAATTTTCAGTAAATGGAGGATCTGTTTCCATTTGGGTGAAAGGA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus parent Termamyl-like alpha-amylase DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48481
uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP
                                                                                                                                                                                                                                                                           1207 GATTATTTTGACCATCATAATATAATCGGATGGACACGTGAAGGAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Termamyl-like alpha-amylase"
                                                 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                                                                                                                                   leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus; alpha-amylase; washing; textile desizing;
starch liquefaction; saccharification; mutein; mutant;
enzyme stability; hybrid; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAA48481 standard; DNA; 1455
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/product=
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314
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407 151

SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl

hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr

13

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ΰ
 Andersen
 Bisgard-Frantzen H,
 ŝ
Kjaerulff
                     WPI; 2000-387777/33.
 Svendsen A,
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P-PSDB; AAY99603

one tiant of parent termamyl-like alpha amylase useful for washing, tile desizing and starch liquefaction, comprising alterations in more solvent exposed amino acid residues Variant of textile

English Disclosure; Page 66-67; 80pp; The present sequence encodes a parent Termamyl-like alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacilius genomic DNa library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the industrial processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing dishwashing and textile desizing. Hybrid alpha-amylases alpha-amylases have also been created in order to increase enzyme

Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

Gaps: 2 Percent Identity: 66.460 Length: Quality: 1860.50 Ratio: 4.327 Milarity: 89.027 US-09-590-375-1 x AAA48481 Percent Similarity: alignment_scores: alignment_block

to: 1455 from: 1 Align seg 1/1 to: AAA48481

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs

nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 17

TGATGGGAATCACTGGAATAGATTAAGAGATGATGCTAGTAATCTAAGAA 106 27

84

134 aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT TGTCGAGGTGAATCCAAATAACCGGAATCAAGAAATATCTGGGGACTACA 406

431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447

1006 1056 347 381 806 331 181 281 297 1057 TATGCGCTTATTTTAACAAGAACAAGGCTATCCCTCTGTCTTCTATGG nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs 607 TATGCAGATGTAGATATGGATCATCCGGAGGTAGTAGAAGTTAGAAG sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 1007 CTGGGGAATCATTAGAATCATTTGTACAAGAATGGTTTAAGCCACTTGCT yAspTyrTyrGly1leProAsnAspAsnIleSerAlaLysLysAspMetI ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 348 381 557 198 248 757 807 281 298 907 314 957 331 364 1157 398 1207 457 167 507 182 231 264

alignment_scores

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The present sequence encodes a parent alpha-amylase from which mutants with increased stability at acidic pH, low calcium concentration and high temperatures have been derived. The sequence was isolated from a Bacillus genomic DNA library. A variant may contain mutations in one or more solvent exposed amino acid residues to increase the overall hydrophobicity of the enzyme or the overall number of methyl groups in the side chains of exposed residues may be increased. The mutations can be incorporated by site-directed mutagenesis or by random mutagenesis. As a result of their increased stability, the variants are suitable for the saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variant of parent termamyl-like alpha amylase useful for washing, textile desizing and starch liquefaction, comprising alterations in one or more solvent exposed amino acid residues
464
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                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA48486
                                                                                    AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 70-71; 80pp; English.
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1..1455
/*tag a /product= "Termamyl-1/partial
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ID AAA48486 standard; DNA; 1455 BP.
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Sequence 1455 BP; 473 A; 227 C; 352 G; 403 T; 0 other;

to increase enzyme stability.

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206
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                                                                                                                                                                                                                                                                                                                                                         eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG .84
                                                                                                                            1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17
                                                                                                                                                       7 AATGGGACAAATGGGACGATGCAATACTTTGAATGGCACTTGCCTAA
                                                                                                                                                                                   17 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA
                                                                                                                                                                                                                                                                                                                 34 spAlaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGGAT
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| ATGGGGAGAATGGTATACAAATACATTAAATCTTGATGGATTTAGGATCG
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                             Percent Identity: 66.460
  Length:
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Ouality: 1860.50
Ratio: 4.327
Harity: 89.027
                                                                                               Align seg 1/1 to: AAA48486
                                                      alignment_block:
US-09-590-375-1 x AAA48486
                          Percent Similarity:
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P-PSDB; AAB30701
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                                                                                                                         WO200075344-A1
                                                                misc_feature
                                                                                         misc_feature
                                                                                                                                                                           02-JUN-1999;
                                         misc_feature
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                        sig_peptide
                                                                                                                                          14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
DNA encoding a Bacillus pectate lyase and JP170 alpha-amylase fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pectate lyase; pectinase; alpha-1,4-glycosidic linkage; pectic acid; polygalacturonic acid; alpha-amylase; ss.
                                                                                                                                                                                                                                           S57 AAAGCATCCAATGCATGCCGTAACTTTTGTGGATAATCACGATTCTCAAC 1006
                                                                                                                                                  364
                                                                                                                                          347
                                                                                                                                                                                                                                                                                                                                                                                                                        907 AGTGGAGGCAACTATGACATGGCAAAACTTCTTAATGGAACGGTTGTTCA 956
                                                                                                                                                                                                          yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
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                                                                                                                                                                                                                                                                                                                                                                               AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
                                                                                                                                                                                                                                                                                                                                                                                                               pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
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                                                 etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
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                                                                                                                                          roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                                                                                                          348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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The present sequence encodes a fusion protein of a Bacillus pectate lyase polypeptide and a JP170 alpha-amylase polypeptide. Pectate alpase is a pectinase which catalyses the random cleavage of alpha-1,4-glycosidic linkages in pectic acid (polygalacturonic acid). The fusion polypeptide is expressed using the cells of the invention. The specification describes a cell for improved production of a fusion protein comprising a native pectate lyase fused to an exogenous polypeptide. The cell is preferably a gram positive cell. The cell is polypeptides, which have been difficult to obtain, such as active human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus cells having a DNA sequence coding for a pectate lyase, a proteolytic cleavage target site, or a polypeptide of exogenous origin fused sequentially into one open reading frame, for producing fusion proteins in higher yields
/product= "Bacillus pectate lyase and JP170 alpha-amylase fusion"
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Gaps: 2
Percent Identity: 66.460
                                                                                                                                /*tag= c
/note="encodes pectate lyase"
1036.1047
/*tag= d
/note="encodes IEGR linker"
1048.2502
                                                                                                                                                                                                                                                                                                    /*tag= e
/note= "encodes alpha-amylase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2000; 2000WO-DK00296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99DK-0000780
99US-0138692
                                                                                *tag= b
                                                                                                          88..1029
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Ratio: 4.327
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US-09-590-375-1 x AAC86598
                                                      1..87
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1154 ATAGAGGIATAACCGCTATTTGGATTCCGCCTGCCTGGAAGGGACTTCG 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||||::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::||:::|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
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                                                                luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
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Alkaline liquefying alpha-amylase; Bacillus; alpha-amylase; detergent; starch-related polysaccharide; hydrolysis; enzyme; surfactant resistance; alpha-1,4-glucosidic link; alkalophilic Bacillus; laundry detergent; dish-washing detergent; starch; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding alkaline liquefying alpha-amylase - useful in dish-washing and laundry detergents for removal of starch dirts
                2354 GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 2403
                                                                                                                                                                        /product= alkaline liquefying alpha-amylase
                                                                                                                                                                                                                                                               447
                                                                                                                                                                                                             431
                                                                                                                                                                                                                                                                                                                 464
                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT51339
                                                                                                                                                                                                         1154 TGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAGCCAAGA
348 TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
                                                  364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                                                                     381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
                                                                                                                    AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
                                                                                                                                                                                                                                                            431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr
                                                                                                                                                                                                                                                                                                               AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding sequence for alkaline liquefying alpha-amylase.
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145..1695
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ID AAT51339 standard; DNA; 1776 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-JP01641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             species KSM-AP1378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ara K, Hatada Y, Ito S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
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P-PSDB; AAW11326.
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                                                                                                                                                                                                                                                                                                               448
                                                                                                                                                        398
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alpha-amylase. Alpha-amylase is an enzyme that acts on starch related polysaccharides, hydrolysing the alpha-1,4-glucoside bond of the polysaccharide molecule. Alkaline liquefying alpha-amylases exhibit resistance to surfactants used in detergents, and decompose starch or starch-related polysaccharides in a highly random manner. The Bacillus species KSM-AP1378, from which this sequence was isolated, is an alkalophilic Bacillus strain. It was isolated from soil in the vicinity of the city of Tochigi. The enzyme is useful in improving the efficiency of dish-washing and laundry detergents, particularly on starch dirts.
                                                                            This sequence represents the coding sequence for an alkaline liquefying
                      Page 23-26; 40pp; English
                      Claim 8;
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Sequence 1776 BP; 575 A; 305 C; 417 G; 479 T; 0 other

Percent Identity: 66.874 Quality: 1853.50 Ratio: 4.300 Percent Similarity: 89.234 alignment_block: US-09-590-375-1 x AAT51339 alignment_scores:

Gaps: Length:

to: 1776 from: 1 Align seg 1/1 to: AAT51339

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs

34 nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 11

20 34 spalaGlyIleThralalleTrplleProProAlaTyrLysGlyAsnSer

GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 51

443

150 hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 134

SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167 TCCAACTTTAAATGGCGCTGGTATCATTTTGATGGGACAGATTGGGATCA 151 694

181 n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn.... 167

..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197 182

GTGCGTAACACCACAGGTAAACCAATGTTTGCAGTTGCAGAATTTTGGAA 1043 AGTGGTGGCTATTTTGATATGAGAAATATTTTAAATGGTTCTGTCGTACA 1193 AAAACACCCTATACATGCAGTCACATTTGTTGATAACCATGACTCTCAGC 1243 CTCCCACCCAAATTCAGGACTTGCAACTATTATGTCCGATGGGCCAGGGG 1543 GTAATAAATGGATGTATGTCGGGAAACATAAAGCTGGCCAAGTATGGAGA 1593 431 247 sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM 281 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381 AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414 464 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264 GGGGAATTTCACTGTAAACGGAGGGGCAGTTTCGGTTTGGGTGAAGCAA 1692 GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln ualaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP : |||||||::|||||||||||||| 381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr CATGGGACTGGGAAGTAGATATAGAGAACGGCAACTATGATTACCTTATG TATGCAGACATTGATATGGATCATCCAGAAGTAATCAATGAACTTAGAAA TTGGGGAGTTTGGTATACAAATACACTTAAATCTAGATGGATTTAGAATCG roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla TGATTACTACGGTATACCAACTCATGGTGTTCCTTCGATGAAATCTAAAA spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln||||||:::|||| :::|||| 844 1044 1144 1194 1244 1294 1344 1394 1444 1494 1544 1594 894 248 264 281 298 348 398 414 431 198 214 231 994 314 331 364 464

seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2000.DAT:AAC66234 seq_documentation_block:

803 197 214 903 231 953 247

AAC66234;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
                                                                                                                                     SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl 167
                                                                                                                                                                                                                                            n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
                                                                          aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT
                                                                                                                                                                                                   ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu
                                                                                                                                                                                                                                                                                                                        GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs
                                                                                                                                                                                                                                                                                                                                                                                     854 TATGCAGACATTGATATGGATCATCCAGAAGTAATCAATGAACTTAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spalalleLysHisIleProPheTrpTyrThrSerAspTrpValArgHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sAspAspValGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etSerLeuPheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyralaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a mutant alpha-amylase. Included in the invention are a gene encoding the mutant alpha-amylase, a vector containing the gene, and a transformed cell recombined by the vector. The enzyme is used in a detergent composition. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                      novel mutant alpha-amylase for use in a detergent composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1786 BP; 578 A; 307 C; 420 G; 481 T; 0 other;
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Percent Identity: 66.874
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                                                                                           Mutant alpha-amylase nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents the mutant alpha-amylase gene.
                                                                                                                          Alpha-amylase; detergent; Bacillus;
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 6-9; 12pp; Japanese.
   ВР
 DNA; 1786
                                                                                                                                                                                                                                                    99JP-0048213
                                                                                                                                                                                                                                                                                 99JP-0048213
                                                             (first entry)
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Ratio: 4.300
Percent Similarity: 89.234
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US-09-590-375-1 x AAC66234
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AAC66234 standard;
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                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB35714
                                                                                                                                                                                      JP2000245466-A.
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                                                             19-FEB-2001
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..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
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TATGCAGACGTGGATATGGATCACCCCAGAAGTAATACATGAACTTAGAAA
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                                                                                                                                                                                                                        GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh
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Ouality: 1835.50
Ratio: 4.319
ilarity: 87.992
                                                                                                                                                         to: AAT00776
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                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New alkaline Bacillus alpha-amylase - used in e.g. detergent compsns. starch liquefaction, textile desizing, starch modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-amylase; enzyme; EC-3.2.1.1; detergent; surfactant; textile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen MD;
                                         1454 GATTATTTTGATCATCATGATATTATCGGCTGGACGAGGGGGACAG 1503
                                                                                                                                                    GATATCACCGGAAATAGGTCTGGTACCGTCACCATTAATGCAGATGGTTG 1653
                                                                                                                                                                                                                      464
                                                                                                                               lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
                                                                                                                                                                                                                                                                                                                                                    GGGGAATTTCACTGTAAACGGAGGGCCAGTTTCGGTTTGGGTGAAGCAA 1702
                                                                                                                                                                                                                                                                                                           pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:AAT00776
                                                                                                                                                                                                                      AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sp. alkaline alpha-amylase DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
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ID AAT00776 standard; DNA; 1455
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94DK-0000353.
94DK-0001271.
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beer; starch;

Bacillus.

16-MAR-1996

AAT00776;

W09526397-A1

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Van DER ZEE

03-FEB-1995; 29-MAR-1994; 03-NOV-1994;

29-MAR-1995;

05-OCT-1995

or beer making

Sequence 1455

alignment_scores:

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to: 1455

from: 1

Percent Identity: 66.253 Gaps: Length:

256 100 406

456 167 506 181 556 909 214

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sp. matur sp. matur

Fotal number of

Searched:

88

Minimum Maximum ••

Database

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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Liquefying alpha-amylase; detergent; starch industry; brewing industry; pharmaceutical industry; food industry; fibre industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New liquefying alkaline amylase, useful in a detergent composition comprises a residual activity of not less than 70 % when treated under specific conditions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus sp. liquefying alpha-amylase #2.
                                                                                           AAB29337
AAB29336
AAB29321
                                                                                                                                                                                                                                      AAB29384
AAB29370
AAB29371
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AAB29332
AAB29368
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AAB29351
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AAB29373
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AAB29378
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AAB29383
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AAB29323
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                                        AAB29338
                                                     AAB29339
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98JP-0362488.
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N-PSDB; AAA70314.
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21-DEC-1998;
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RESULT
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                                                                                                                           2687 |
1 DGLNGTMMQYYEWHLENDGQ......GDGWGEFFTNGGSVSVYVNQ 480
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Bacillus sp.
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/SIDSZ/gcgdata/geneseq/geneseqp/AA1990 .DAT: *
/SIDSZ/gcgdata/geneseq/geneseqp/AA1990 .DAT: *
/SIDSZ/gcgdata/geneseq/geneseqp/AA1991 .DAT: *
/SIDSZ/gcgdata/geneseq/geneseqp/AA1993 .DAT: *
/SIDSZ/gcgdata/geneseqp/geneseqp/AA1994 .DAT: *
/SIDSZ/gcgdata/geneseqp/geneseqp/AA1995 .DAT: *
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Compugen Ltd.
                                                                                                                                                                                                               hits satisfying chosen parameters:
                                                                                                                                                                                           522463 seqs, 74073290 residues
         GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                       November 28, 2001, 16:54:37
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Maximum Match 100%
Listing first 45 summaries
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AAB29341
AAB29345
AAB29346

    protein search, using sw model

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AAB29318
AAB29342
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Gapop 10.0 , Gapext 0.5
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                    The present sequence is a novel alpha-amylase from Bacillus sp. The invention concerns the isolation of two new liquefying alpha-amylases from Bacillus sp. strains KSM-KSB and KSM-KSB, designated KSG and KSB, which this protein is one. The present alpha amylases are chelating-agent resistant and thus are useful in the starch, brewing, fibre, pharmaceutical and food industries, and especially as components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liquefying alpha-amylase; detergent; starch industry; brewing industry; pharmaceutical industry; food industry; fibre industry.
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                                                                                                                                            1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                                                                                                                   LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV
                                                                                                                                                                                                          NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQRYQENHIFRFANT
                                                                                                                                                                                                                 NWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFWY
                                                                                                                                                                                                                                                241 TSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQGG
                                                                                                                                                                                                                                                                              SYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYPN
                                                                                                                                                                                                                                                                                                               VFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNSG
                                                                                                                               ö
                                                                                                               Length 501;
                                                                                                                               Indels
                                                                                                              Score 2687; DB 21;
Pred. No. 6.6e-214;
                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liquefying alpha-amylase #1.
        Page 17-19; 34pp; English.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                             Conservative
                                                                                                                     Similarity
                                                                                      501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1022334-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1999;
                                                                                                                            Matches 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000,
                                                                        detergents
        Claim 4;
                                                                                      Sequence
                                                                                                             Query Match
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                                                                                                                     Local
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The present sequence is a novel alpha-amylase from Bacillus sp. The invention concerns the isolation of two new liquefying alpha-amylases from Bacillus sp. strains KSM-K36 and KSM-K38, designated K36 and K38, of which this protein is one. The present alpha-amylases are chelating-agent resistant and thus are useful in the starch, brewing, fibre, pharmaceutical and food industries, and especially as components of
                                                                                                                                                          New liquefying alkaline amylase, useful in a detergent composition comprises a residual activity of not less than 70 % when treated under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFWY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 lydlgefngkgtvrtkygtkaqleraigslksndinvygdvvmnklgadfteavgavgv 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQGG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                                           Ozaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQRYQENHIFRFANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 VFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNSG
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                                                                           Κ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2618; DB 21;
Pred. No. 3.3e-208;
13; Mismatches 4;
                                                                           Igarashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus sp. mature alpha-amylase SEQ ID
                                                                       Hayashi Y,
                                                                                                                                                                                                                                 Claim 4; Page 14-16; 34pp; English.
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96.58;
 98JP-0362488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 96.5
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                                                                     Kitayama
                                                                                                                                                                                                specific conditions
                                                                                                       2000-516014/47
                                                                                                                                                                                                                                                                                                                                                                                                                  501 AA;
                                   (KAOS ) KAO CORP.
                                                                                                       WPI; 2000-516014/
N-PSDB; AAA70313
21-DEC-1998;
                                                                     Haqihara H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 463;
                                                                                                                                                                                                                                                                                                                                                                           detergents
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nuclear caides encoding them. The novel alpha-amylases (AAB29311) have improved wash performance in alkaline detergent solutions (PH 9-11) and have a temperature optimum in the range 55-65 degrees (Calsius at pH 9-0.7). The invention also relates to mutents (AAB2918 BAB934) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally according the anglases active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleac acids encoding the appha-amylases of the the invention, and the recombinant production of alpha-amylases of the the invention, in a desizing composition. The alpha-amylases are useful in a detergent composition or a dishwashing or starch, or for ethanol production. In particular, the holp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a ceptergent at alkaline pH. The alpha-amylases are also useful for sequences AAB29311-B29394 represent the mutant Bacillus alpha-amylases
                                alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides having alpha-amylase activity and nucleic acids oding the enzymes, useful as a detergent or a dish wash detergent position, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nielsen VS;
                                                                                                                                                                                                                                                                                                                                                 /note= "Any amino acid other than Arg"
       DSM 12651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Borchert TV,
Andersen C;
   Alpha-amylase; AAI-6; AAI-10; DSM 12650;
                                                                                                                                                                                                                                                      Location/Qualifiers
181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nielsen BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000WO-DK00147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99DK-0000438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-686938/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ethanol production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             483 AA;
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                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200060058-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding the
composition,
                                                                                                                                                                          Bacillus sp. Synthetic.
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textile desizing;
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                                                                                                                                                                                                                                                          New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                      123 npgnrngevsgtyeieawtgfnfpgrgnghssfkwrwyhfdgtdwdgsrglsnriykfxg 182
                                                                            180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW 239
                                                                                                                                                                   GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant, del-D183/G184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alkaline detergent composition; starch liquefaction; textile desizibrewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                         240 YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
                                                                                                                                                                                                                NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nielsen VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nielsen BR, Borchert
Svendsen A, Andersen C;
                                                                                                                                                                                                                                                                                                                                                                                 AAB29318 standard; Protein; 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page -; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000WO-DK00147.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoeck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outtrup H, Hoeck LH
Bisgard-Frantzen H,
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Score 1920.5; Pred. No. 1.4e-3; Mismatches

71.5%; 69.2%;

63;

Conservative

Similarity

Query Match Best Local Simi Matches 333;

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Length 483;

21;

DB

61 LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120

DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60 (first entry)

09-FEB-2001

AAB29342;

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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB20310-B29311) have improved wash performance in alkaline detergent solutions (PH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 59.0. The invention also relates to mutants (AAB20318-B29394) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the contructs and host cells comprising nucleic acids encoding the contructs and host cells comprising nucleic acids encoding the these enzymes. The alpha-amylases are useful in a desizing composition of the alpha-amylases are useful for textile desizing, starch modification for alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, and constability are accepted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              especially useful for removing starchy stains during washing with a detergent at alkaling pure paracelly useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AABS9318-B29330 represent specific embodiments of the mutant Bacillus alpha-amylases of the invention.

Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AABS9310) shown on page 105-106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shown on page 105-106.
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                                                                                   LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                                NPTNRWQDISGAYTIDAWIGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                                          299
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                                                                                                                                                                                                                                                                     NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS 419
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                                                                                                                                                                                                                                                                                                                                              420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
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                                            DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                       180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW
                                                                                                                                                                                     YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
                                                                                                                                                                                                                                                           GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP
                                                                                                                                                                                                                                                                                                                 ];
     Length 483;
 71.4%; Score 1919.5; DB 21; Lengt 69.2%; Pred. No. 1.7e-150; Live 63; Mismatches 84; Indels
Query Match
Best Local Similarity 69.28
Matches 333; Conservative
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29311) have improved wash performance in alkaline detergent solutions (pH 9-11) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9.0. The invention also relates to mutants (AAB29318-B29344) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally acceded to a compasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of alpha-amylases are useful in a detergent composition or a dishwash detergent composition, in a desizing composition or a dishwash detergent composition, in a desizing starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are specially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for secondary stains during washing or industrial ethanol from starch or whole grains. Sequences AAB2931-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                 Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is not shown in the specification, but be wild-type Bacillus sp. alpha amylase (AAB29310)
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                                                                                                 mature alpha-amylase SEQ ID NO:2 mutant #12.
                                                                                                                                                                                                                                                                                                                                /note= "Any amino acid other than Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Borchert TV,
Andersen C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nielsen BR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2000; 2000WO-DK00147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DK-0000489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Outtrup H, Hoeck LH,
Bisgard-Frantzen H, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-686938/67.
                                                                                                                                                                                                                                                                                                              Misc-difference 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from the
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                                                                                             Bacillus sp.
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                                                                                                                                                                                                                                   Bacillus sp.
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                                                                                                                                                                                                                                                       Synthetic.
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Length 483;

Score 1915.5; DB 21; Pred. No. 3.7e-150;

71.3%;

Best Local Similarity

Query Match

AAB29342 standard; Protein; 483 AA.

RESULT
AAB29342
ID AAB29

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420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TIWWINWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 YISDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
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                                                                                                                                                                                                                   419
                                                        LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                 NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW 239
                                                                                                                                                           GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP 359
                                                                                                                                                                                          Gaps
               DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                        240 YISDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
                                                                                                                                                                                                                  NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Any amino acid other than Val"
                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
85;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                           AAB29343 standard; Protein; 483
62;
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus sp.
Synthetic.
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Matches 333;
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9.0. The invention also relates to mutants (AAB29318-B29394) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructs and host cells comprising nucleic acids anytaxes, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing composition, in the pulp and paper industry, for brewing or baking, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at allahaline plu. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for ethanol production -
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Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29310) shown on page 105-106.
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69.2%; Pred. No. 3.7e-150;
ive 62; Mismatches 85;
ပ်
    Andersen
                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page -; 112pp; English.
Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.3'
Best Local Similarity 69.2'
Matches 333; Conservative
Bisgard-Frantzen H,
                                                                             WPI; 2000-686938/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to two novel Bacillus alpha-amylases, AAI-6 from 2C Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and not nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9.0. The invention also relates to mutants (AAB29318-B29394) of the covel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally constructs and host cels comprising nucleic acids encoding the acidic pH and/or at low Ca2+ concentration. The invention additionally constructs and host cels comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition of the alpha-amylases are useful in a desizing composition. Cor a dishwash detergent composition, in a desizing composition of starch, or for ethanol production. In particular, for late than anylases are useful for textile desizing, starch modification dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a cespecially useful for removing starchy stains during washing with a producting drinking or industrial ethanol from starch or whole grains.
                                                                                                                                                                                                                                                         Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for ethanol production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nielsen
                                                                                                                                                                                                                                 mature alpha-amylase SEQ ID NO:4 mutant #10.
                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Any amino acid other than Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nielsen BR, Borchert TV, vendsen A, Andersen C;
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                         AAB29372 standard; Protein; 483 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DK-0000438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2000; 2000WO-DK00147
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoeck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outtrup H, Hoeck LH
Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-686938/67.
                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060058-A2
                                                                                                                                                                                                                              Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
13-APR-1999;
                                                                                                                                                                                                  09-FEB-2001
                                                                                                                                                                                                                                                                                                                               Bacillus sp.
Synthetic.
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                                           Q 480
                                                                      483 r 483
                                                                                                                                                                        AAB29372;
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                                                                                                                              AAB29372
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Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                                                                                                                                                                                                                                               LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                                                                                                                                                                                                                                                                                                                   121 NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 qvfygdyygipsdgypsyrqqidpllkarqqyaygrqhdyfdhwdvigwtregnashpns 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                          1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                                                                                                                                                                                                                                                                    of the invention.

Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29311) shown on page 109-110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus sp. mature alpha-amylase SEQ ID NO:4 mutant, del-D183/G184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP
                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                  21; Length 483;
                                                                                                                                                                                                                                        87; Indels
                                                                                                                                                                                         71.3%; Score 1915.5; DB 2
69.2%; Pred. No. 3.7e-150;
iive 60; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB29325 standard; Protein; 483 AA.
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 333; Conserv
                                                                                                                                 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060058-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 r 483
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                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB29325;
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                                                                                                                                                                                                                                                                                                                                                                 61
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gnydmrnllngtlvgrhpshavtfvdnhdtqpgealesfvggwfkplayatiltreggyp 362
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   303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB29341
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                                                                                                                                                                                                                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29310-B39311) have improved wash performance in alkaline detergent solutions (pH 9-11) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9-0. The invention also relates to mutents (AAB2918-B9394) of the encompasses active fragments of movel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally concentructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of alpha-amylases are useful in a detergent composition, or a dishwash detergent composition, in a desizing composition, correct the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are composition and the pulp and paper industry for brewing or baking, or as laundry, conspected at alkaline pH. The alpha-amylases are also useful for removing starchy stains during washing with a ceptergent at alkaline pH. The alpha-amylases are also useful for modification. Consequences AAB29318-B3330 represent specific embodiments of the mutant sequence is not shown in the specification, but the consequence is not shown in the specification, but the consequence is not shown in the specification, and the consequence is not shown in the specification.
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                                                                                                                                                                                                                                                                                                                             New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Length 483;
                                                                                                                                                                                   Nielsen VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87; Indels
                                                                                                                                                                                , Borchert TV,
Andersen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1914.5; DB 21
Pred. No. 4.4e-150;
60; Mismatches 87;
                                                                                                                                                                                   BR,
                                                                                                                                                                                                            Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page -; 112pp; English.
                                                                                                                                                                                Nielsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.3%;
69.2%;
                            99DK-0000438.
99DK-0000489.
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                                                                                                                    (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shown on page 109-110
                                                                                                                                                                                Hoeck LH,
                                                                                                                                                                                                                                                                 WPI; 2000-686938/67.
                                                                                                                                                                                                            Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                        ethanol production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      483 AA;
                            31-MAR-1999;
13-APR-1999;
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                                                                                                                                                                                Outtrup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (ABAB29110-B29311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9.0. The invention also relates to mutants (ABAB2918-B2934) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition or a dishwash detergent composition, in a desizing composition.
                                                                                                                                                                                                                                                                                                                                                                                                      Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                     New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for ethanol production -
                                                                    GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
                360 NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nielsen VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Any amino acid other than Val"
                                                                                                                                                                                                                                                                                                                                                                         mature alpha-amylase SEQ ID NO:2 mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Svendsen A, Andersen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borchert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                 AAB29341 standard; Protein; 483 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2000; 2000WO-DK00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99DK-0000489
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                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-'686938/67.
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Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                       Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-1999;
                                                                                                                                                                                                                                                                                                                                     09-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000.
                                                                                                                                       480 Q 480
                                                                                                                                                                          r 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Synthetic

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for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-amylase; AAI-6; AAI-10; DSW 12650; DSW 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                   LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                          121 NPTNRWQDISGAYTIDAWTGEDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                        DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60
                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                     Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29310) shown on page 105-106.
                                                                                                                                                                                                                                                                                                                                                                                     180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
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                                                                                                                                                                                                                                                  DB 21; Length 483;
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                                                                                                                                                                                                                                               71.3%; Score 1914.5; DB 2. 69.2%; Pred. No. 4.4e-150;
                                                                                                                                                                                                                                                                             62; Mismatches
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Best Local Similarity 69.2%
Matches 333; Conservative
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                                                                                                                                                                                                    483 AA;
                                                                                                                         of the invention.
Note: The present
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB23310-B2311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 5.0. The invention also relates to mutants (AAB23318-B29394) of the covel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition, for a dishwash detergent composition, in a desizing composition. The pulp amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or Daking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a recombing or a taking varied and alpha-amylases are also useful for removing starchy stains during washing viewed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
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                                                                                                                                                                                                                                                                                                                    Nielsen VS;
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                                                                        /note= "Any amino acid other than Glu"
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Andersen C;
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i, Mismatches 85;
                              ney Location/Qualifiers
Misc-difference 210
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99DK-0000489.
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Best Local Similarity
Matches 332; Conserv
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13-APR-1999;
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363 420 123

AAB29348 standard; Protein; 483 AA. Best Local Similarity 69.03 Matches 332; Conservative 483 AA; the invention. 480 Q 480 r 483 AAB29348; Sequence Query Match 12 19 121 123 420 483 AAB29348 g ò g ŏ g à qq ò a 셤 ò ŏ δ g ò ò 셤 The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein. 419 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479 New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP 360 NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS Nielsen VS; Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #16. /note= "Any amino acid other than Glu" , Borchert TV, Andersen C; Location/Qualifiers AAB29346 standard; Protein; 483 AA. Nielsen BR, Svendsen A, Claim 21; Page -; 112pp; English. 99DK-0000438. 28-MAR-2000; 2000WO-DK00147 (first entry) (NOVO) NOVO NORDISK AS. Hoeck LH, Bisgard-Frantzen H, WPI; 2000-686938/67 ethanol production Misc-difference WO200060058-A2 31-MAR-1999; 13-APR-1999; 09-FEB-2001 Bacillus sp. Synthetic. 12-OCT-2000 Outtrup H, 480 Q 480 483 r 483 AAB29346;

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nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311)
have improved wash performance in alkaline detergent solutions (pH 9-11)
and have a temperature optimum in the range 55.65 degrees Celsius at pH
condition also relates to mattants (AAB29318-B2934) of the
novel alpha-amylases having increased thermal stability, particularly at
acidic pH and/or at low Ca2+ concentration. The invention additionally
constructs and host calls comprising nucleic acids encoding the
alpha-amylases of the the invention, and the recombinant production of
these enzymes. The alpha-amylases are useful in a detergent composition
or a dishwash detergent composition, in a desizing composition,
for liquefaction of starch, or for ethanol production. In particular,
the alpha-amylases are useful for textile desizing composition,
in the pulp and paper industry, for brewing or baking, or as laundry,
dishwashing or hard surface cleaning detergent compositions. They are
especially useful for removing starchy stains during washing with a
ceptergent at alkaline pH. The alpha-amylases are also useful for
producing drinking or industrial ethanol from starch or whole grains.
Sequences AAB2931-B29394 represent the mutant Bacillus alpha-amylases
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69.0%; Pred. No. 5.3e-150;
ive 63; Mismatches 85;
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09-FEB-2001

Bacillus sp

Synthetic.

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Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergrent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479
                    DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD
                                                                                        LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV
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Svendsen A, Andersen C;
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Bisgard-Frantzen H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB23310-B3311) have improved wash performance in alkaline detergent solutions (pH 9-11) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees (Calsius at pH 9-10). The invention also relates to mutants (AAB23318-B29340) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and haramylases are useful in a detergent composition or a dishwashing or bard surface cleaning detergent composition. In particular, the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for sequences AAB2931-B29394 represent the mutant Bacillus alpha-amylases
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                                                                                                    Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651; alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h . 71.2%; Score 1913.5; DB 21; Length 483; Similarity 69.0%; Pred. No. 5.3e-150; Conservative 63; Mismatches 85; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nielsen VS;
                                                       Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #18
                                                                                                                                                                                                                                                                                                                          /note= "Any amino acid other than Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Borchert TV,
Andersen C;
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bisgard-Frantzen H, Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2000; 2000WO-DK00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DK-0000438
99DK-0000489
             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoeck LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-686938/67
                                                                                                                                                                                                                                                                                                     Misc-difference 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ethanol production
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31-MAR-1999; 13-APR-1999;

Outtrup H,

12-OCT-2000

Nielsen VS;

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Sequence

Query Match Best Local &

AAB29351 standard; Protein; 483 AA.

AAB29351;

δλ q 14

AAB29351

WPI; 2000-686938/67.

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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB231310-B3311) and have a temperature optimum in the range 55-65 degrees (Esius at pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9-0. The invention also relates to mutants (AAB2318 B29344) of the ovel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Ca2+ concentration. The invention additionally concendases active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells comprising nucleic acids encoding the constructs and host cells composition, in a desizing composition or a dishwash detergent composition, in a desizing composition or a dishwash detergent composition, in a desizing composition or the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for sequences AAB29318-B29394 represent the mutant Bacillus alpha-amylases
                                               polypeptides having alpha-amylase activity and nucleic acids oding the enzymes, useful as a detergent or a dish wash detergent ossition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the invention.
Le: The present sequence is not shown in the specification, but derived from the wild-type Bacillus sp. alpha amylase (AAB29310)
                                                                                                                                                                                   Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shown on page 105-106.
                                                                                                                                   ethanol production
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                                                                                                 composition,
                                                                           encoding
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ä LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120 NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179 TNWNWRYDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW 239 YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG 299 363 qvfygdyygipsdgvpsyrqqidpllkarqqyaygrqhdyfdhwdvigwtregnashpns 422 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN 479 1; Gaps 1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD 60 GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS 85; Indels 71.2%; Score 1913.5; DB 21; 69.0%; Pred. No. 5.3e-150; ive 63; Mismatches 85; In Conservative Similarity Matches 332; Query Match Best Local 180 240 121 123 303 360 셤 g ð 셤 ò 8 g ò g à ò 셤 ò ò ò

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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB23310-B3311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 5.0. The invention also relates to mutants (AAB29318-B29394) of the covel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Cast concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition, or a dishwash detergent composition, in a desizing composition, or for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, in the pulp and paper industry, for brewing or baking, or as laundry, in the pulp and paper industry, for brewing or baking with a detergent at alkaline pH. The alpha-amylases are also useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for scucing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases

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alkaline detergent composition; starch liquefaction; textile desizing; brewing; baking; ethanol production; starch modification; laundry; dishwashing; surface cleaning; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                         New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for
                                                                                                                                                                                                                                                                                           Nielsen VS;
                                              Bacillus sp. mature alpha-amylase SEQ ID NO:2 mutant #21.
                                                                                                                                                                /note= "Any amino acid other than Lys"
                                                                 Alpha-amylase; AAI-6; AAI-10; DSM 12650; DSM 12651;
                                                                                                                                                                                                                                                                                          Borchert TV,
                                                                                                                                                                                                                                                                                                    Bisgard-Frantzen H, Svendsen A, Andersen C;
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                          Nielsen BR,
                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page -; 112pp; English.
                                                                                                                                                                                                                         28-MAR-2000; 2000WO-DK00147.
                                                                                                                                                                                                                                           99DK-0000438.
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                                                                                                                                                                                                                                                                        (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                          Outtrup H, Hoeck LH,
                                                                                                                                                                                                                                                                                                                       WPI; 2000-686938/67.
                                                                                                                                                       Misc-difference 267
                                                                                                                                                                                                                                                                                                                                                                      ethanol production
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13-APR-1999;
                            09-FEB-2001
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                                                                                                                 Bacillus sp
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                                                                                                                                       NPTNRWQDISGAYTIDAWTGFDFSGRNNAYSDFKWRWFHFNGVDWDQ-RYQENHIFRFAN 179
                                                                                                                                                                          242
                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                     359
                                                                                                                                                                                                                                                                                        362
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                                                                                                                                                                                                                                                                                                                                                  LYDLGEFNQKGTVRTKYGTKAQLERAIGSLKSNDINVYGDVVMNHKMGADFTEAVQAVQV 120
                                                                              Gaps
                                                                                               9
                                                                                                      Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29310) shown on page 105-106.
                                                                                              1 DGLNGTMMQYYEWHLENDGQHWNRLHDDAAALSDAGITAIWIPPAYKGNSQADVGYGAYD
                                                                                                                                                                                                  180 TNWNWRVDEENGNYDYLLGSNIDFSHPEVQDELKDWGSWFTDELDLDGYRLDAIKHIPFW
                                                                                                                                                                                                           GSYDMRNILRGSLVEAHPMHAVTFVDNHDTQPGESLESWVADWFKPLAYATILTREGGYP
                                                                                                                                                                                                                                                                               420 GLATIMSNGPGGSKWMYVGRQNAGQTWTDLTGNNGASVTINGDGWGEFFTNGGSVSVYVN
                                                                                                                                                                                                                                    240 YTSDWVRHQRNEADQDLFVVGEYWKDDVGALEFYLDEMNWEMSLFDVPLNYNFYRASQQG
                                                                                                                                                                                                                                                                                                        NVFYGDYYGIPNDNISAKKDMIDELLDARQNYAYGTQHDYFDHWDVVGWTREGSSSRPNS
                                                                                                                                                                                                                                                                                                                       363 qvfygdyygipsdgvpsyrqqidpllkarqqyaygrqhdyfdhwdvigwtregnashpns
                                                            DB 21; Length 483;
                                                          71.2%; Score 1913.5; DB 21; Lengt
69.0%; Pred. No. 5.3e-150;
ive 63; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mature alpha-amylase SEQ ID NO:2 mutant #22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Any amino acid other than Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
267
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB29352 standard; Protein; 483 AA
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                                                                             Conservative
                                                           Query Match
Best Local Similarity
Matches 332; Conserv
                                  483 AA;
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The invention relates to two novel Bacillus alpha-amylases, AAI-6 from Bacillus sp. DSM 12650, and AAI-10 from Bacillus sp. DSM 12651, and nucleic acids encoding them. The novel alpha-amylases (AAB29310-B29311) have improved wash performance in alkaline detergent solutions (pH 9-11) and have a temperature optimum in the range 55-65 degrees Celsius at pH 9-0. The invention also relates to mutants (AAB29318-B39344) of the novel alpha-amylases having increased thermal stability, particularly at acidic pH and/or at low Cat-concentration. The invention additionally encompasses active fragments of the novel alpha-amylases, expression constructs and host cells comprising nucleic acids encoding the alpha-amylases of the the invention, and the recombinant production of these enzymes. The alpha-amylases are useful in a detergent composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or a dishwash detergent composition, in a desizing composition, for liquefaction of starch, or for ethanol production. In particular, the alpha-amylases are useful for textile desizing, starch modification in the pulp and paper industry, for brewing or baking, or as laundry, dishwashing or hard surface cleaning detergent compositions. They are especially useful for removing starchy stains during washing with a detergent at alkaline pH. The alpha-amylases are also useful for producing drinking or industrial ethanol from starch or whole grains. Sequences AAB29331-B29394 represent the mutant Bacillus alpha-amylases
                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides having alpha-amylase activity and nucleic acids encoding the enzymes, useful as a detergent or a dish wash detergent composition, for textile desizing, for liquefaction of starch, or for ethanol production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The present sequence is not shown in the specification, but is derived from the wild-type Bacillus sp. alpha amylase (AAB29310) shown on page 105-106.
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Pred. No. 5.3e-150;
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Andersen C;
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69.0%;
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28-MAR-2000; 2000WO-DK00147
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Bisgard-Frantzen H,
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Best Local Similarity
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                                                            31-MAR-1999;
13-APR-1999;
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AZ686517 ENTSR71R Entamoeba
AV834558 AV834558 K. Sato un
BI265677 NF08380951NIF1077 In
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| Location/Qualifiers |
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| Ab_Large="maxpace" |
| Alab_bost="E. coli DH10B" |
| Alab_bost="E.
                                                                                                                                                                                                          seq_documentation_block:

LOCUS AQ159619 768 bp DNA GSS 09-SEP-1998

DEFINITION mgxb0001K09r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0001K09r, DNA sequence.

ACCESSION AQ159619

VERSION AQ159619.1 GI:3556644
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Budaryota; Fungil. Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertee sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 768)
1. Y. Y. Zhu H., Boyd,C. A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Clemson.edu
Clemson.edu
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gb_gss:AZ686517
gb_est1:AV834958
gb_est2:BI265677
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A0155619 MGNDOOLKODY CUGI Rice
BF648570 NF016C06DT1F1039 Droug
BF648570 NF0476C0EDIF1039 Droug
BF648570 NF047620 CVCI III
BF647944 NF047608PL1F1056 Phosp
BF647949 NF07F12EC1F1098 Elici
AW709933 d9060e. £I Neurospora
AL13781 Anopheles gambiae GSS
BF79139 L48-278673 LCC Plus
BF29366 WHE2156 el0 12025 Trit
BF29366 WHE2156 el0 12025 Trit
BF29366 WHE2156 el0 12025 Trit
BF29348 HVSMEf0001E16f Hordeum
BF011027 SE233 SUGAT Beet gampiae B1073204 PIP2B G10 SUGAT Beet
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6 AU083906 Cryptomeria J
8 MEST33-H04.T7-1 ISUM3-
13 WHE2151_E01_10125 Trit
8 Kr3-C8 Sugar Beet ger
9 WHE2166_A01_B0225 Trit
6 EST425835 potato leave
6 EST425835 potato leave
8 DG1_50_H11.b1_A002 Dar
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4 DG1_148_D01.b1_A002 Da

9 EST516520 CSTD Solanum

5 EST40773 tomato break

0 DG1_61_C11.b1_A002 Dar

9 EST412238 tomato break
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| B117333 RE1623.5prime RE Dros
| BF293134 WHE2164_A02_A0425 Trit
| BF29375 WHE2157_B10_D192S Trit
| BF644049 NF089G07EC1F1056 Elici
| BE360816 DG1_67_F11.b2_A002 Dar
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EST407651 tomato break
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Arabidopsis thaliana
                                                                                                                                                                                                        -MODEL-frame+p20.model -DEV=x1h
-Q=Cqn2_1/USPTO_spool/US09590375/runat_28112001_152037_21046/app_query.fasta_1.1092
-Q=Cqn2_1/USPTO_spool/US09590375/runat_28112001_152037_21046/app_query.fasta_1.1092
-DB=EST _OFMT-fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-QGAPEXT=0.100 -LOOPCL=0.000 -LOOPEXT=0.500 -FGAPOP=6.000
-QGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
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-DELEXT=7.000 -YGAPOP=10.000 -YGAPOP=0.TRANS=humand/0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -TRANS=humand/0.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCT -TRANS=HUMAND-THR_MIN=0
-ALIGN=15 -MOGE=COALIGN=200 -THR_SCORE=PCT -TRANS=100 -THR_MIN=0
-ALIGN=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY
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AW777164
                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_est1:BE360066
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gb_est1:BE460819
gb_est2:BE3607373
gb_est2:BE36573
gb_est2:BE36573
gb_est2:BE36573
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gb_est2:BF647599
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gb_gest2:BF479139
gb_est2:BF793866
gb_est2:BF793866
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gb_est2:BF793894
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gb_est1:AW777164
gb_est1:BF8932879
gb_est2:BF8932879
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gb_est2:BF632036
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Thu Nov

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Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF632036 639 bp mRNA EST 19-DEC-2000 MRN4C016C06DT1F1039 Drought Medicago truncatula cDNA clone NF016C06DT 5', mRNA sequence.
BF632036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPheSerGlyArgAsnAsnAlaTyrSerAspPheLysTrpArgTrpPheH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 isPheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsnHisIlePhe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||::::::||||::
652 TCTGAAGTCAGGAGTGAGTTCTTAAAGTGGCCCCAAGTGGCTCAACGATCA 701
                                                                                                                                                                   LeuLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLy 106
                                                                                                                                                                                                                                                   sMetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProT 123
                                                                                                                                                                                                                                                                               202 GGCCGGCGCGGATTCCACCGAGCGATGCTTGCCACGAGGGTGGACCAG 251
                                                                                                                                                                                                                                                                                                                                                                                                                         206 ProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAspGl 222
                                        52 CGACGTCTACGATCTGTATGATCTGGGCCAGTTTGACCAGAAAGGCTCCA 101
                                                                                                         152 GCGGGGGACGCCGCCATTGAGATCCTGTTTGATGCCGTGCTGAACCACAA 201
                                                                                                                                                                                                                                                                                                                                                                              252 AGGGTTTGTGCCCTGATTGTTGCCATGGGCAAGATGCCGTTGTATCGCAT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            502 TTGTTTGAGGGCAAGAAGTGGGCCCGAGGATGTGAACGGGGAGTTTGGTAA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 CTATGACTACCTGTGAGTCTCGAGTGTCGGAGATGTTTCTCGACGGTGCC 601
rGlyalaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrV 73
                                                                                 73 alArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySer 89
                                                                                                                                                                                                                                                                                                                                                                                                                                              302 CGCGGCTGACAAAAAAAAACTGCCACGGTACTCCTTGATGTTGCAGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CGCANACAGGTCGATCGCCCGGGAGAGATCGAGGCGTGGACCAAGTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 ArgPheAlaAsnThrAsnTrpAsnTrpArgValAspGluGluAsnGlyAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......LeuGlySerAsnIleAspPheSerHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCCTAAATTTGATGCTATCAGAATGGTTGCAGACCTAGATCATTCACAT
                                                                                                                                                                                                                                                                                                                                  123 hrAsn.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....IleAspAlaTrpThrGlyPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222 uLeuAspLeuAspGlyTyrArgLeuAspAlaIleLysHisIle 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF632036.1 GI:11896194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:BF632036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 TyrThr.....
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T AUTHORS
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KEYWORDS
  26
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Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains a mixture of entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entinplantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::|||:::|||||||
176 TTGGCTTCCTCCT.....CCATCTCAAAGTGTTGGTCCTCAAGGATAT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 CTCTTTCAGGGATTCAACTGGGAGTCAAGTAACAAAGGAGGATGGTACAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 CTCTTTGAAGAACCTCATTCCTGACCTAGCAAATGCTGGAATTACACATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 .GCATCAAAATACGGTTCAAAAGATGACCTAAAGTCACTAATTGCAGCTT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAAAGATAAAGGAATCAATTGTCTAGCTGACATAGTGATCAACCATAGA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnProTh 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nArgLeuHisAspAspAlaAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 lArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
                                                                                                                                Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7331
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 639 Std Error: 0.00
Plate: 016 row: C column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 leTrplleProProAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 CTTCCAGGAAGACTTTATGATCTTGAT..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 233
Gaps: 13
Percent Identity: 30.043
                                                                                                                                                                                                                                                                                                                                                                                                                                               truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="NF016C06DT"
/clone_lib="Drought"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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                                                                                Unpublished (2000)
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1.718
53.219
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                                                                                                               Contact: May GD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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seq_documentation_block:
LOCUS BG581061 558 bp mRNA EST 11-APR-2001
DEFINITION EST482791 GVN Medicago truncatula cDNA clone pGVN-63M12 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 GlnAspGluLeuLysAspTrpGlySerTrpPheThrAspGluLeuAspLe 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : CTCATTCCTGACCTAGCAAATGCTGGAATTACACATGTTTGGCTTCCTC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 CTTTATGATCTTGAT......GCATCAAATA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spileAsnValTyrGlyAspValValMetAsnHisLysMetGlyAlaAsp 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 .....ACAGCAGAAAGAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 erGlyArgAsnAsnAlaTyrSerAspPheLysTrpArgTrp.PheHis.P 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 heAsnGlyValAspTrpAspGlnArgTyrGlnGluAsnHis...IlePhe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 ArgPheAlaAsnThrAsnTrpAsnTrpArg.ValAspGluGluAsnGlyA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491
                                                                                                                                                                                                                                               87 ITCAACTGGGAGTCAAGTAACAAAGGAGGATGGTACAACTCTTTGAAGAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGTTCAAAAGATGACCTAAAGTCACTAATTGCAGCTTTCAAAGATAAAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 nAspIleSerGlyAlaTyrThrIleAspAlaTrpThrGlyPheAspPheS 144
                                                                                                                                                                                                                                                                                                                                                                                                                               || ::::::|| CATCTCAAAGTGTTGGTCCTCAAGGATGTTCCAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 TyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAsnArgLeuHisAs
                                                                                                                                                                                                                                                                                                27 pAspAlaAlaLeuSerAspAlaGlyIleThrAlaIleTrpIleProP
                                                                                                                                                                                                                                                                                                                                                                                                roAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyrGlyAlaTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rGlyThrLysAlaGlnLeuGluArgAlaIleGlySerLeuLysSerAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 PheThrGluAlaValGlnAlaValGlnValAsnProThrAsnArgTrpGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....TTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||| :::
388 AAGGT......GGGACTCCTGATTCAAACTTGATTGGGGCCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....TIGCAAAGAIGACACTGCTTAITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 .....TATCAAGCTGCACCTGACATTGATCATCTCAATCCTCAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrValArgThrLysTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 snTyrAspTyrLeuLeuGlySerAsnIleAspPheSerHisProGluVal
Gaps: 12
Percent Identity: 29.386
                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::::|||:::|||| :::|||| :::|||| 584 TTCTGGGTGGAGATTTGATTTTGTCAAA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 AGATGATAGAGGCATCTATTGCCTC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 uAspGlyTyrArgLeuAspAlaIleLys 234
                                                                                                                                                   from: 1
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BG581061
BG581061.1 GI:13596125
1.775
52.632
                                                                                                                                                to: BF648578
                                                                     alignment_block:
US-09-590-375-1 x BF648578
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                    Percent Similarity:
                                                                                                                                                Align seg 1/1
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VERSION
KEYWORDS
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/tissue_type="Cell suspensions were subcultured every 14
days.cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Fabales; Fabaceae; Papillonoideae; Trifolleae; Medicago.

1 (bases 1 to 665)

1 (bases 1 to 665)

1 (bases I.K. Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF047602EC1F1019 Elicited cell culture Medicago truncatula cDNA clone NF047G02EC 5', mRNA sequence.
                                                                                                                                                                          204
.....TITGAAGGT......GGGACTCCTGATTCAAAACTTGAT 417
                                              157 Trp.PheHis.PheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsn 172
                                                                                                                                                173 His...IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValAspG 188
                                                                                                                                                                                                                                                                                                                                                                         523 AATCCTCAAGTACAAAAAGAGTTATCTGAATGGATGATTGGCTCAAAAC
                                                                                               ...TTGCAAAGATGA
                                                                                                                                                                                                                                               188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer
                                                                                                                                                                                                                                                                                              482 GIGGAGAGGC.....IATCAAGCTGCACCTGACATTGATCATCTC
                                                                                                                                                                                                                                                                                                                                            HisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 pGlu.LeuAspLeuAspGlyTyrArgLeuAspAlaIleLys 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: radixon@noble.org
Insert Length: 665 Std Error: 0.00
Plate: 047 row: G column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                               418 IGGGCCCCATCTTTCAT
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SOURCE
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GCATCAAAATACGGTTCAAAAGATGACCTAAAGGTCACTAAAGTTGCAGCTT 244
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1. 587
/organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 pGluLeuAspLeuAspGlyTyrArgLeuAspAlaIle 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF637944.1 GI:11902102
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//dev_gtage="affective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
//dab_host="E. coll strain XLOLR"
//dab_host="E. coll strain XLOLR"
//note="Vector: pBluescript SK-; Site_1: ECORI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The CDNA was directionally ligated into the Unit ZAP XR vector from Stratagene and packaged using Glagapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                  Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                             Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M382117e TIGR sequence name:
WTCDD78TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA ApA CTA gtg gAT CC).
Location/Qualifiers
                                         Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                    St.Paul, MN 55108 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 nArgLeuHisAspAspAlaAlaAlaLeuSerAspAlaGlyIleThrAlaI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 leTrpIleProProAlaTyrLysGlyAsnSerGlnAlaAspValGlyTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyThrVa 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 lArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs
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                                                                                                                                                                                                               truncatula, 2001
Unpublished (2001)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, 37 Feb. (61-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 231
Gaps: 12
Percent Identity: 29.004
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  barrel medic.
Medicago truncatula
                                                                                                                               (bases 1 to 558)
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1.744
52.381
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US-09-590-375-1 x BG581061
                                                                                                           Medicago
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF637944 587 bp mRNA EST 19-DEC-2000 NF041C08PL181056 Phosphate starved leaf Medicago truncatula cDNA clone NF041C08PL 5', mRNA sequence.
BF637944
                                          245 TCAAAGATAAAGGAATCAATTGTCTAGCTGACATAGTGATCAACCATAGA 294
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                                                                                                                                                                                                                                                                                            123 rAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpThrG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                             140 lyPheAspPheSerGlyArgAsnAsnAlaTyrSerAspPheLysTrpArg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....TITGAAGGT......GGGACTCCTGATTCAAAACTTGAT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trp.PheHis.PheAsnGlyValAspTrpAspGlnArgTyrGlnGluAsn 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TTGCAAAGATGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 His...IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValAspG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 luGluAsnGlyAsnTyrAspTyrLeuLeuGlySerAsnIleAspPheSer 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 GTGGAGGGC.....TATCAAGCTGCACCTGACATTGATCATCT 471
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euLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLys
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Contact: Harrison MJ
Plant Balogy Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7335
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 887 Std Error: 0.00
Plate: 041 row: C column: 08
Seq primer: TCACACAGGAAACAGCTAATGAC.
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FEATURES
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/tissue_type="leaf"
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/dev_stage="trifoliate"
/dev_stage="trifoliate"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
fruncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoadlands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 CTCTTTCAGGGATTCAACTGGGAGTCAAGTAACAAAGGAGGATGGTACAA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 His...IlePheArgPheAlaAsnThrAsnTrpAsnTrpArg.ValAspG 188
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                                                                                                                                                                                                                                                                                                                                                                      Length: 229
Gaps: 12
Percent Identity: 29.258
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/db_xref="taxon:3880"
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1.744
52.838
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US-09-590-375-1 x BF637944
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                          172
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                                                                                                                                                                                                                                                        BASE COUNT
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                                                                                                                                                                                                                                                                                   ORIGIN
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/clone_lib" Elicited cell culture"
//clone_lib" Elicited
/tissue_type="Cell cultures derived from root tissues"
/tessue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
the concentration. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
129 c 125 g 197 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula
bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 635)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research
Unpublished (2000)
                                                                                                                                                                                                                                                                                seq_documentation_block:

LOCUS BF647599 635 bp mRNA EST 20-DEC-2000
DEFINITION WF077E12EC1F1098 Elicited cell culture Medicago truncatula cDNA
clone WF077E12EC 5', mRNA sequence.

ACCESSION BF647599 GI:11912729
                                205 HisProGluValGlnAspGluLeuLysAspTrpGlySerTrpPheThrAs 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 TrpHisLeuGluAsnAspGlyGlnHisTrpAsnArgLeuHisAspAspAl 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 aAlaAlaLeuSerAspAlaGlyIleThrAlaIleTrpIleProProAlaT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 635 Std Error: 0.00
Plate: 077 row: E column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 226
Gaps: 12
Percent Identity: 29.646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF077E12EC"
                                                                                                                                                                     556 TGAAATTGGATTTTCTGGTTGGAGATTTGAT 586
                                                                                                             221 pGluLeuAspLeuAspGlyTyrArgLeuAsp 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210.00
1.780
52.212
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US-09-590-375-1 x BF647599
                                                                                                                                                                                                                              seq_name: gb_est2:BF647599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS
AW709933
436 bp mRNA
DEFINITION
d9b06ne.fl Neurospora crassa evening cDNA library Neurospora crassa
CDNA clone 69b06ne 5', mRNA sequence.
ACCESSION
AW709933.1 GI:7599010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurospora crassa
Eukaryota: Fungi: Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sordariales, Sordariaceae; Neurospora.

1 (bases I to 436)
Thu, Kupfer 1. Dunlap, J.C. and Roe, B.A.
Thu Neurospora crassa EST Databases
Unpublished (1998)
Other_ESTS: d9b06ne.11
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
G20 Parrington Oval, Norman, OK 73019, USA
145 TCCTGACCTAGCAAATGCTGGAATTACACATGTTTGGCTTCCTCCT.... 190
                                                                                  191 ..CCATCTCAAAGTGTTGGTCCTCAAGGATATCTTCCAGGAAGACTTTAT 238
                                                                                                                                                                           239 GATCTTGAT.....GCATCAAAATACGGTTC 264
                                                                                                                                                                                                                                                                                                                                                                                             113 GluAlaValGlnAlaValGlnValAsnProThrAsnArgTrpGlnAspIl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 eSerGlyAlaTyrThrIleAspAlaTrpThrGlyPheAspPheSerGlyA 146
                                                                                                                                                                                                                                                  snValTyrGlyAspValValMetAsnHisLysMetGlyAlaAspPheThr 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 rgAsnAsnAlaTyrSerAspPheLysTrpArgTrp.PheHis.PheAsnG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 lyValAspTrpAspGlnArgTyrGlnGluAsnHis...IlePheArgPhe 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 AlaAsnThrAsnTrpAsnTrpArg.ValAspGluGluAsnGlyAsnTyrA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 spTyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAsp 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                .....ACAGCAGAAAAGATGA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 rLysAlaGlnLeuGluArgAlaIleGlySerLeuLysSerAsnAspIleA 96
                                         46 yrLysGlyAsnSerGlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyr
                                                                                                                                63 AspLeuGlyGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyTh
                                                                                                                                                                                                                                                                                                                                                  315 ATTGTCTAGCTGACATAGTGATCAACCATAGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 GluLeuLysAspTrpGlySerTrpPheThrAspGluLeuAspLeuAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ......GGGACTCCTGATTCAAAACTTGATTGGGGCCCATCTTTCAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592 TTGGAGATTTGATTTTGTCAAA 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 yTyrArgLeuAspAlalleLys 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
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ORGANISM
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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                           347
                                                                                                                                                                                                                                                                                                           96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seg primer: Universal Forward Primer
High quality sequence stop: 424.
                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:
ECORI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into EcoRI site of pBluescript"
159 c. 93 g 102 t
                                                                                                                                                            1. .436
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/db_xref="taxon:1141"
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/clone=lib="Neurospora crassa evening cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSOIOCL 681 bp DNA GSS 14-JUN-2001
Anopheles gambiae GSS T7 end of clone 26N13 of Notrebamel library
from strain PEST of Anopheles gambiae (African malaria mosquito),
AL153781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 PheValValGlyGluTyrTrpLysAspAspValGlyAlaLeuGluPheTy 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 yrasnPheTyrarg.................AlaSerGln 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 CCAACTTCTCCCGCATCTTTAGCTTCCGAACACCTCCAAGCCTCTCCC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 ACCGGTGGTGGTGGTGCTCCCGGGATCACGTACGGCAGCCGCGACAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 rAspMetArgAsnIleLeuArgGlySerLeuValGluAlaHisProMetH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 CGACCTCCGCACCTTATTCGACGACACCCTCTGCATCTGGAAACCGCACA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 GlnGlyGly....SerTy 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206.50 Length: 119
2.950 Gaps: 2
58.824 Percent Identity: 41.176
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AW709933
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment block:
                                                                                                                                                                 source
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ORGANISM

KEYWORDS SOURCE

VERSION

AUTHORS TITLE JOURNAL

REFERENCE

TITLE JOURNAL AUTHORS

COMMENT

FEATURES

REFERENCE

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/organism="mesembryanthemum crystallinum"
/db_xref="taxon.3544"
/db_xref="taxon.3544"
/db_xref="taxon.3544"
/clone_lib="L48-2786"
/flone_lib="Ice plant Lambda Uni-Zap XR expression library
/ 48 hours NaCl treatment"
/fissue_type="Leaf, 48 h 0.4m NaCl"
/des_stage="Six week old"
/note="vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: Xhol"
                                         BF479139 712 bp mRNA EST 20-FEB-2001
L48-2786T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-2786
                                                                                                                                                                             common ice plant.

Mesembryanthemum crystallinum

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 712)

Cushman, J.C.
                                                                                                                                                                                                                                                                                                                                               An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum Unpublished (1997)
Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AsnTrpAsn...TrpArgVal.....AspGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 PheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleLysHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 GATTGGGGTCCTTGGTCCATTTGCAGGGACGACACACAATACTCCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySerTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 uAsnGlyAsnTyrAsp.....TyrLeuLeuGlySerAsnIleA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 13
Percent Identity: 28.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
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Seq primer: T3
High quality sequence stop: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MS200, Reno, NV 89557-0014,
Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 g
                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                    BF479139.1 GI:11549966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jcushman@unr.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 c
                                                                                                        5', mRNA sequence.
BF479139
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1.523
54.167
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                    seq_documentation_block:
LOCUS BF479139
DEFINITION L48-2786T3 IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD:
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KEYWORDS
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                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
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                                                                                                                                                                    Genoscope.

Direct Submission
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EFW cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
2 (bases 1 to 681)
                                                                                                                                                                                                                                                                                                   Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                               Eukāryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidea; Anopheles.
I (bases 1 to 681)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 ACCTGTG.CTGCCGCCTGCCTACAAGGGGGGTTCCGGCGGCTACTCCGTC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||::::::|||::::|||304 ACCCTGCTGCTATCTTCCATGGTACTTACCCCGACGCCGCAAACTGTG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 lySerLeuLysSerAsn..AspIleAsnValTyrGlyAspValValMetA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAsnArgLeuHisAspAspAlaAlaAlaLeuSerAspAlaGlyIleThrA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 GlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGl 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 yThrValArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ThrMetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 lalleTrplleProProAlaTyrLysGlyAsnSerGlnAla...AspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: CNS0100L from: 1 to: 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 102
Gaps: 2
Percent Identity: 46.078

    681
    organism="Anopheles gambiae"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="PEST"
/db.xref="taxon:7165"
/clone="26N13"
/clone_11b="NotreDame1"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 g
                                      African malaria mosquito.
AL153781.1 GI:7014700
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2.704
74.510
                                                             Anopheles gambiae
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 ACCAC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
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BASE COUNT

ORIGIN

22

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Fax:
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Triticum turgidum.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;

Triticeae; Triticum.

( bases I to 533)

Adhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J.,

Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R.,

Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS BF293666 533 bp mRNA EST 17-NOV-2000
DEFINITION WHE2156_e10_i2028 Triticum turgidum L. var. durum (durum wheat)
whole plant cDNA library Triticum turgidum cDNA clone
WHE2156_e10_i20, mRNA sequence.
ACCESSION BF293666 1 GI:11224730
235 sIleProPheTrpTyrThrSerAspTrpValArgHisGlnArgAsnGluA 252
                                                                                                                                         374 GACTAGGTGGGTGCAAGCTGCTGGCAGAGGCGTTGCCACTGCATTTGATT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                           ... TyrArgAlaSerGlnGlnGlyGlySerTyrAsp 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 TCACCACAAAGGGAATTCTTCAAGCTGCCGTTCAAGGAGAATGGTGGAGA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetArg.....AsnIleLeuArgGlySerLeuValGluAlaHisProMe 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 tHisAlaValThrPheValAspAsnHisAspThrGlnProGlyGluSerL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euGluSerTrpValAlaAspTrpPheLysProteu...AlaTyrAlaThr 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGlyAspTyr.. 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....TyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetIleA 382
                                                         .........GAGG 273
                                                                                                                                                                                                                    ... AspvalGlyAlaLeuGluPheTyrLeuAspGluMetAsnTrpGluMe 281
                                                                                                                                                                                                                                                                             324 GGACAAGATGGGAAACCAAACTATAATCAAGATTCACATAGATATGAGCT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             568 AAAAGTTTTGGCCATTCCCATCTGATAAAGTTATGCAAGGATATGCCTAT 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....AAGGATGAAATTG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 laAspGlnAspLeuPheValValGlyGluTyrTrpLysAsp.....
                                                                                                                                                                                                                                                                                                                                 tSerLeuPhe..........AspValProLeuAsnTyrAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 ATGAAAGACTCCAATGGCAAGCCAAGTGGAATGATAGGAGTTTTACCACA
                                                   239 ATATGCGCCTAGCATAACAAGATTTACATG...
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and Zhang,D.
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AUTHORS
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KEYWORDS
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sequence and low 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 GluAlaValGlnAlaValGlnValAsnProThrAsnArgTrpGlnAspIl 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 aAlaAlaLeuSerAspAlaGlyIleThrAlaIleTrpIleProproAlaT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GluAsnAspGlyGlnHisTrpAsnArgLeuHis.....AspAspAl 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 AspLeuGlyGluPheAsnGlnLysGlyThrValArgThrLysTyrGlyTh 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 rLysAlaGlnLeuGluArgAlaIleGlySerLeuLysSerAsnAspIleA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AGGCCATCGCCGACATCGTCAACCACCGC........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 yrLysGlyAsnSerGlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyr
                        Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 237
Gaps: 10
Percent Identity: 27.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 533
                                                                  Location/Qualifiers
             Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.836
45.148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: BF293666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196.50
5105595818
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US-09-590-375-1 x BF293666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                    97
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HVCDNA0007 (etiolated and unstressed)" /tissue_type="Seedling root" /lab_host="TJC121" /note="Vector: lambda2AP; Site_1: EcoR1; Site more details on library preparation and seques see http://www.genome.clemson.edu/projects/boorder a clone see http://www.genome.clemson.unstream	alignment_scores: Quality: 195.00	7 MetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGlnHisTrpAs 23 :::::: :::::	36 lylleThralalleTrplleProProAlaTyrLysGlyAsnSerGlnAla 52	accardcarccaccrcarcaccacarccac nLysGlyThrValargThrLysTyrGlyThrLysAlaGlnLeuGluArgA i:: :: :: :: :: ::	103 MetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAlaValGl 119 ::: :: 312 ATCAACCGCTGCGCCGACTAC	136 spAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyrSerAsp 152 :::	169 rGlnGluAsnHisIlePheArgPheAlaAsnThrAsnTrpAsnTrpArgy 186 111:::::::::::::::::::::::::::::::::
129 eSerGlyAlaTyrThrIleAspAlaTrpThrGlyPheAspPheSerGlyA 146	CCGCGA hrasnT Tyrasp GCCGAC	195 TyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAspGl 211 :::::::	228 yrArgLeuAsp 231 :: :: 519 GGCGCTTCGAC 529 seq_name: gb_est2:BF253388	seq_documentation_block: LOCUS LOCUS BF253388 616 bp mRNA EST 23-FEB-2001 DEFINITION HVSMEf0001E16f Hordeum vulgare seedling root EST 11brary HVCDNA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0001E16f, mRNA sequence. ACCESSION BF253388 VERSTON BF253388 2 GI:13116477 KEYWORDS EST OCHANTEN HORDERS		TITLE Development of a genetically and physically anchored EST resource for barley genomics JOURNAL Unpublished (2000) COMMENT On Nov 16, 2000 this sequence version replaced gi:11182589. Contact: Wing RA Clemson University Genomics Institute Clemson University Genomics SC 29634, USA	Tel: 864 656 4298 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: AATTAACCTCACTAAAGG High quality sequence stop: 517. FEATURES 1. 616 /organism="Hordeum vulgare" //orlivar="Morex" /db_xref="taxon:4513" //clone="HVSMEf0001E16f" //clone="HVSMEf0001E16f"

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nbda2AP; Site_1: EcoR1; Site_2: Xho1; For
ibrary preparation and sequence analysis
nome.clemson.edu/projects/barley/ To
http://www.genome.clemson.edu/orders"
1 106 t
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36C.....389
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|GACATCGAC......224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |||:::|||:::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCGACTGGGGCCCC.... 404
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ted and unstressed)"
ling root"
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Gaps: 9
Identity: 25.764
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208 TAATICCCICAAAACTCAAICGAIGAITIGGCICGAGCAGGGGTIACAC 257
  pAsnArgLeuHisAspAspAlaAlaAlaLeuSerAspAlaGlyIleThrA 39
                                                                                                                                                                                                                                             302 TATATGCCAGGAAGATTATATGATCTTGATTCA.
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                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllades; Caryophyllades; Caryophyllades; Chenopodiaceae; Beta.

[ (bases 1 to 71)
de los Reyes, B.G., McGrath, J.M., Myers, S. and Derrico, C.
Differential gene expression in sugar beet seedlings (Beta vulgaris)
germinated under stress conditions
Unpublished (2000)
Contact: J. Mitchell McGrath
                                                                                                                                                            58233 Sugar Beet germination cDNA library Beta vulgaris cDNA clone ys016f795's similar to alpha amylase, mRNA sequence.

BF011027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research
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/clone=lbb="Sugar Beet germination cDNA library"
/tissue_type="whole seedlings"
/dev_stage="4-day germination under stress (salt/NaCl, dehydration/Mannitol and anaerobic stress)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michigan State University
494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
791 (517)-432-2355
Fax: (517)-337-6782
Email: mitchmcg@pilot.msu.edu
Seq primer: T3
High quality sequence stop: 750.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 9
Percent Identity: 25.573
219 eThrAspGluLeuAspLeuAspGlyTyrArgLeuAsp 231
                           545 TCAGAGGGACCTCAGCTTCGACGCGTGGCGCCTTGAC 581
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US-09-590-375-1 x BF011027
                                                                                             seq_name: gb_est2:BF011027
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TITLE
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COMMENT
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BI073204 702 bp mRNA EST 19-JUN-2001
PIPSDE-G10 Sugar Beet germination CDNA library Beta vulgaris CDNA 5'
similar to alpha amylase, mRNA sequence.
BI073204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 GTAGTGGAAATCTAGACACTGGAGCTGGTTATGGTGCTGCTGATATA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 GCTCAAGACAGAAATTGGTTTTGACGGATGGAGAGTTTGATTTGTTAAGG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 ArgTrpPheHisPheAsnGlyValAspTrpAspGlnArgTyrGlnGluAs 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 nHisIlePheArgPheAlaAsnThrAsnTrpAsnTrpArgValAspGluG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 pPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaIleLysH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATATGCTCCTAGCATTACCAAAATTTACATGGAAAAAACTAGGCCTGAT 748
                                             .....TCTAGATACGGGAATGAGGCTGATCTGAAGAGCTTGATTAATG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                        erLeuLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHis 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 CCTTCCACCAAAAAGGAATCAAAAGTGTTTGCTGATATAGTTATAAATCAT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysMetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnPr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 AGATGC...GCAGAT..... 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 hrGlyPheAspPheSerGlyArgAsnAsnAlaTyrSerAspPheLysTrp 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....TTCGAAGGCGGAACTCCAGATGACCGCCTAGATTGNGG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 luAsnGlyAsnTyrAsp.....TyrLeuLeuGlySerAsnIle 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 AspPheSerHisProGluValGlnAspGluLeuLysAspTrpGlySerTr 218
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39 laIleTrpIleProProAlaTyrLysGlyAsnSerGlnAlaAspValGly 55
                                                                                                                                               TyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyTh 72
                                                                                                                                                                                                                                                                                           72 rValArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlyS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 .....AAGAAAGATGGAAGAAGATATACTGTATT
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AQ159694 743 bp DNA GSS 09-SEP-1998
mgxb0001108r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
clone mgxb0001108r, DNA sequence.
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Phillips,K., Sasinowski,M. Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnaporthe grisea.
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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100 Jordan Hall, Clemson Universiy, Clemson, SC 29634
Tel: 864 656 5737
Fax: 864 656 4228
Email: rdean@clemson.edu
Seq primer: GGAAACAGCTATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...TyrLeuLeuGlySerAsnIleAspPheSerHisProGluValGlnAs 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 CCTTCCACCAAAAAGGAATCAAATGTGTTGCGGATATAGTGATAAATCAT 382
                                                        LysMetGlyAlaAspPheThrGluAlaValGlnAlaValGlnValAsnPr 122
                                                                                                                                                 122 oThrAsnArgTrpGlnAspIleSerGlyAlaTyrThrIleAspAlaTrpT 139
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                                                                                                                                                                                                                                                                                                                                         ArgTrpPheHisPheAsnGlyValAspTrpAspGlnArgTyrGlnGluAs 172
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                                                                                                                                                                                                                                                                                                                                                                       .....AAGCAAGATGGTAGAGGAATCTATTGTATA.....
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/strain="70-15"
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Clemson University Genomics Institute
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High quality sequence stop: 348.
Location/Qualifiers
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Yu,Y., Zhu u
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Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
1 (bases 1 to 702)
de los Reyes,B.G., McGrath,J.M. and Myers,S.
Differential gene expression in sugar beet seedlings (Beta vulgaris ) germinated under stress conditions (de los Reyes,B.G., McGrath
                                                                                                                        ,J.M., Myers,S.)
Unpublished (2001)
Contact: J. Mitchell McGrath
Sugar Beet Genetics Lab., USDA/ARS/Sugar Beet and Bean Research
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Beta vulgaris"
/cultivar="USH20"
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/clone_lib="Sugar Beet germination cDNA library"
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/dev_stage="4-day germination under stress (salt/Nacl, dehydration/Mannitol and anaerobic stress)"
                                                                                                                                                                                                              Unit
Michigan State University
494 Plant and Soil Sci. Bldg., East Lansing MI 48824, USA
Tel: (517)-432-2355
Fax: (517)-337-6782
Email: mitchmcg@pilot.msu.edu
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 TATCTTCCTGGAAGATTGTATGATCTTGAT.....286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 ....GCATCTAGATATGGCAACGGGGCTGATTTAAAGAGCTTGATTAACG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 erLeuLysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHis 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 MetMetGlnTyrTyrGluTrpHisLeuGluAsn...AspGlyGlnHisTr 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 pAsnArgLeuHisAspAspAlaAlaAlaLeuSerAspAlaGlyIleThrA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPheAsnGlnLysGlyTh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 rValArgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlyS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 laIleTrpIleProProAlaTyrLysGlyAsnSerGlnAlaAspValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 241
Gaps: 10
Percent Identity: 26.141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1 to: 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host-"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: BI073204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190.00
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                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                   AUTHORS
TITLE
                             REFERENCE
                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
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                                                                                                                                                                    COMMENT
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source
                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                  REFERENCE
                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                      Accessive to the most devestating fungal diseases of rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (1-7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25% genome coverage. High density colony filters are available upon request." 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW223546 678 bp mRNA EST 18-MAY-2001
EST300357 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573 GAGGGCTCCAGNGCGACCAAGTGGGCCCCCAGGACCGAACTGGACGAGCTC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 LysSerAsnAspIleAsnValTyrGlyAspValValMetAsnHisLysMe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   655 ......ATCCTGTTTGATGCCGTGCTGAACACANGGGC 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 nLys.....GlyThrValA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 rgThrLysTyrGlyThrLysAlaGlnLeuGluArgAlaIleGlySerLeu 90
                   /clone_lib="CUGI Rice Blast BAC Library"
/tissue_type="Protoplasts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAsnAspGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  623 GTTCGCGCGCGGGGGACGCCGGCATTTGAG......
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 3
Percent Identity: 36.441
                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 743
                                                           /lab_host="E. coli DH10B
/clone="mgxb0001108r"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone cLEN12E8, mRNA sequence.
AW223546
AW223546.1 GI:6535230
                                                                                                                                                                                                                                                                                                                                                                                                      188.50
2.856
55.932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AQ159694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-590-375-1 x AQ159694
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                                                                                                                                                                                                                                                                                                    BASE COUNT
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                                                                                                                                                                                                                                                                                                                         ORIGIN
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Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

tomato.

VERSION KEYWORDS SOURCE ORGANISM

```
/issue_type="neartoriang" / dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="vector: pBlueScript SK(+): Site_1: EcoR1; Site_2:
Xhol; supplier: djovannon; Fruit were tagged at the
breaker stage (first sign of lycopene accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fult) and harvested 7 days
post-breaker (over-ripe). 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."
                                                                                 1 (bases 1 to 678)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
Clemson University
110 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 AsnIleAspPheSerHisProGluValGlnAspGluLeuLysAspTrpGl 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 ySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuAspAlaI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 ACTGIGGCTGAGGGAGGAGTTGGTTATGATGGATGGAGGCTTGATTTG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 leLysHisIleProPheTrp.....TyrThrSerAspTrpValArgHis 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 .....GAAGCAACTGAACCTTACTTCGCTGTAGGCGAGTTTTGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....TyrLeuAspGluMetAsnTrpGluMetSerLeu 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheAspValProLeu.....AsnTyrAs 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cLEN12E8"
/clone_lib="tomato fruit red ripe, TAMU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 GGCAGAGAATTATTGACTGGATTAATGCTACTAATGGAACTGCAGGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACATTGATCATTCCCAGGAATTCGTGAGAAAGGATATCAGGGAATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 TTCGT.....GGGTTTTTGGGGTGATGTGAAGGATTACTTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 sAspAspVal.....GlyAlaLeuGluPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 239
Gaps: 12
Percent Identity: 27.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .678
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1.500
52.301
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US-09-590-375-1 x AW223546
                                                              Lycopersicon.
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28	281 TTTGACGTGACAACGAAGGGAATTCTTCATTCTGCAATTGAGAGATGTGA	330
291		308
331	1 ATACTGGCGACTATCCGATCAGAGGGGAAA	361
30	308 euArgGlySerLeuValGluAlaHisProMetHisAlaValThrPheVal	324
362	2CCTCCCGGCGTTGTTGGATGGTGGCCATCTCGTGCTGTTACATTATA	409
325		341
410	GAGAATCATGATACAGGTTCTACACGGGTCATTGGAGATTCC	453
34	1 pTrpPheLysProLeuAlaTyrAlaThrIleLeuThrArgGluGlyG	357
45	454 TGGTGGGAAGAGATGCAAGGTTATGCCTATATCCTGACTCACCCTG	200
357		373
501		532
374		390
533		578
39	O nTyrAlaTyrGlyThrGlnHisAspTyrPheAspHisTrpAspValValG	407
57	579GAACACGATTACCTGTCGGAGTTTGGTGATATC	613
40	407 lyTrpThrArgGluGly 412	
61		

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+ 1723.50 2392.01
+ 1723.50 2392.01
+ 1723.50 2391.98
+ 1723.50 2391.80
+ 1723.50 2391.80
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Ratio: 5.598
Percent Similarity: 100.000
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US-09-590-375-1 x AX137670
                                                                                                                                                                             seq_name: gb_pat:AX137670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
gb_pat:AR137886
gb_pat:AX036890
gb_pat:AR143216
gb_ba:BACAMYS
gb_pat:A91241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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4 from pate
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14 from pate
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AR037274 Sequence I from pater
AR052144 Sequence I from pater
AR087550 Sequence I from pater
AR129915 Sequence 12 from pater
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pate
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AX137672 Sequence 1 from Pat.
AX037040 Sequence 1 from Pat.
AX037042 Sequence 3 from Pat.
AR037042 Sequence 5 from Pat.
AR049518 Sequence 5 from pat.
AR1043913 Sequence 10 from pat.
AR129913 Sequence 10 from pat.
AR129918 Sequence 10 from pat.
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AR13788 Sequence 14 from pat.
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Bacillus sp. KSM-K38
Bacillus sp. KSM-K38
Bacillus Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.

1 (bases 1 to 1753)
Endo, K., Igarashi, K., Hayashi, Y., Hagihara, H. and Ozaki, K. Mutant alpha-amylases
Patent: EP 106277-A 3 03-JAN-2001;
Kao Corporation (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 34
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ACCESSION AX137670
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Bacillus sp. KSM-K36
Bacillus sp. KSM-K36
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 1625)
Endo, K., Igarashi, K., Hayashi, Y., Hagihara, H. and Ozaki, K.
Mutant alpha-amylases
Patent: EP 1065277-A 5 03-JAN-2001;
Kao Corporation (JP)
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DEFINITION Sequence 5 from Patent EP1065277.
VERSION AX137672.1 GI:14273855
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alignment_scores:

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 Length:
                                                                     to: 1625
                                                                     from: 1
        5.477
                                                                     Align seg 1/1 to: AX137672
Quality: 2618.00
                                                 US-09-590-375-1 x AX137672
                   Percent Similarity:
           Ratio:
                                         alignment_block:
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                                               Bacillus Sp.
Bacteria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 o 1458)
Borchert, T.V. 1000, L.H., Outtrup, H., Svendsen, A., Bisgaard-Frantzen, H., Nielsen, B.R. and Nielsen, N.S. Polypeptides having alkaline alpha-amylase activity
                                                                                                                                                                                                                                                                                                                                 euLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHisAspTyrPhe 400
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heAspValProLeuAsnTyrAsnPheTyrArgAlaSerGlnGlnGlyGly
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Patent: WO 0060058-A 112-OCT-2000;
NOVONORDISK AS (DK)
Location/Qualifiers
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290 c 357 g 365 t
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/note="unnamed protein product<sup>†</sup>
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/organism="Bacillus sp.
/db_xref="taxon:1409"
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..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu
                                                   GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs
                                                                                              607 TATGCAGACGTTGACATGAACCATCCTGAAGTCATAAACCG
                                                                                                                              PTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA
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ACGTCATCCGAGCCATGCGGTTACGTTTGTCGATAACCACGACACACAGC 1006
                                                                                                                  hrileAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
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    207 TAACCAAAAAGGAACGGTCCGTACGAAATATGGAACAAAAGCAGAATTAG
                                                                              AACGAGGGATTCGTTCGTTAAAGGCGAACGGGATTCAAGTGTATGGCGAT
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PPAWKGTSQNDVGYGAYDLYDLGEFROKGTYRTKYGTKAELERAIRSLKANGIQVYGD
VVMNHKGGADFTERVQAVEVNPQNRNGEVSGTYQIEAWTGFNFPGRGNQHSSFKWRY
HFDGTDWDQSRQLANRIYKFRODGKAMDWEVDTENGWYDYLWYADVDHDFBYINELN
RWGVWYANTLALLDGFRLDAYKHIKFSFWRDWLGHVBGQTGKNLFAYABYWKNDLGALE
NYLSKTWANTASAFDVPLHYNLYQASNSGNYDMRNLLMGTLVQRHSBARAYTFVDNHDT
QYGEALESFYGGWFRELAYATILTREGGYPQVFYGDYYGISSDGYPSYRQULDFLLKA
RQQYAYGRQHDYFDHWDVIGWTRGGABPNSGLATINSDGPGGSKWMYVGRQKAGEV
                                                                                                                                                                                                                                                                                               Andersen, C.,
                                                                                                                                                                                                                                                                             Bustbert,T.V., Hock,L.H., Outtrup,H., Svendsen,A., Andersen,C., Bisgaard-Frantzen,H., Nielsen,B.R. and Nielsen,V.S. Polypeptides having alkaline alpha-amylase activity and nucleic acids encoding same
                                                                                                  16-NOV-2000
1407 GGGACAATTTTTGTCAACGGTGGTTCCGTCTCCGTATGGGTGAACGA 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 spalaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer 50
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                                                                                                                                                                                                               Bacillus sp.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacteria: Firmicutes; Bacillus/Staphylococcus group; Bacillus.

(bases 1 to 1458)
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293.c 365 g 361 t
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Gaps: 2
Percent Identity: 68.944
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/note="unnamed protein product"
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Patent: WO 0060058-A 3 12-OCT-2000;
NOVONORDISK AS (DK)
Location/Qualifiers
e 1. 1458
//Organism="Bacillus sp."
//db_xref="taxon:1409"
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/protein_id="CAC16494.1"
/db_xref="G1:11226475"
                                                                                              AX037042 1458 bp DNA
Sequence 3 from Patent W00060058
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Ratio: 4.411
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Percent Similarity: 89.441
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US-09-590-375-1 x AX037042
                                      gb_pat:AX037042
                                                                        seq_documentation_block:
LOCUS AX037042
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eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
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Outtrup, H., Bisg.ang.rd-Frantzen, H., stergaard, P.Rahbek, Rasmussen, M. Dolberg and Van Der Zee, P.
Alkaline bacillus amylase
Patent: US 5856164-A 5 05-JAN-1999;
Location/Qualifiers
ASPTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe 414
                                                                               431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
                                                                                                                                                             AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
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Gaps: 2
Percent Identity: 66.460
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Sequence 5 from patent US
AR027255
AR027255.1 GI:5938095
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Percent Similarity: 89.027
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LOCUS AR027255
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Unclassified.
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             hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
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                                                                       GTAGTGATGAACCATAAAGGAGGAGCTGATGCTACAGAAAACGTTCTTGC
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Outrrup, H., Bisg.ang.rd-Frantzen, H., stergaard, P.Rahbek, Rasmussen, M.Dolberg and Van der Zee, P.
Alkaline bacilus amylase
Patent: US 5824531-A 5 20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAGCCAAGA 1156
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AR049518
AR049518.1 GI:6005557
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KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL

FEATURES TITLE

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                                                                                                    luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
                                                                                                                                                           ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
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                                                                                                                                                                                                                                                                                                                                      GlySerAsnIleAspPheSerHisProGluValGlnAspGluLeuLysAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||:::|||:::|||:::|||657 ATGGGAGATGGTAACAATAAATCTTGATGGATTTAGGATCG
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                                           eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
                                                                                                                                                                            hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
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.07 ATAGAGGTATAACCGCTATTTGGATTCCGCCTGCCTGGAAAGGGACTTCG 156
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                                                                                                                                                                                ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl
                                                                                                                                                                                             hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr
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414
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                                    yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                            TGACTACTATGGAATTCCAACACATAGTGTCCCAGCAATGAAAGCCAAGA
                                                                                   381 leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
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Gaps: 2
Percent Identity: 66.460
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1 (bases 1 to 1455)
Bisg.ang.rd-Frantzen, H., Svendsen, A. and
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Patent: US 6093562-A 5 25-JUL-2000;
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LOCUS AR104349 1455 bp DNA
DEFINITION Sequence 5 from patent US 6093562.
ACCESSION AR104349
VERSION AR104349.1 GI:12817057
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1. .1455
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Percent Similarity: 89.027
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US-09-590-375-1 x AR104349
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Unknown.

SOURCE ORGANISM

KEYWORDS

AUTHORS TITLE REFERENCE

JOURNAL

FEATURES

473

BASE COUNT ORIGIN

alignment_scores:

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331 roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla 347
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spalaGlyIleThrAlaIleTrpIleProProAlaTyrLysGlyAsnSer
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Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H.
alpha.-amylase mutants
Patent: US 6187576-A 10 13-FEB-2001;
Location/Qualifiers
1. .1455
                           GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
                                                                                                                                                                                                                                                                                                                                                                                                       TTGATCCAATCTTAGAGGCGCGTCAAAATTTTGCATATGGAACACAACAT 1206
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            348 TyralaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl 364
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                                                                                                                                     7 AATGGGACAAATGGGACGATGCAATACTTTGAATGGCACTTGCCTAA
                                                                          364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                                                                                                                                                                  AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
                                                                                                                                                                                                                                                              rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG
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Gaps: 2
Percent Identity: 66.460
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227 c 352 g
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Sequence 10 from patent US AR129913
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Ratio: 4.327
Harity: 89.027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pat:AR129913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
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Percent Similarity:
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DEFINITION

1307

1357

1407

1257

414

ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

506

167

181 556

406

306

67

84

959

214

231 706 247

909

197

756

264

856

297

alignment_block:

source

FEATURES TITLE

BASE COUNT

ORIGIN

364

381 1157 398

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57 IGAIGGGAAICACIGGAAIAGAITAAGAGAIGAIGCIAGIAAICIAAGAA 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 1455)
Svendsen,A., Borchert,T.Vedel and Bisg.ang.rd-Frantzen,H. alpha.-amylase mutents
Patent: US 6187576-A 15 13-FEB-2001;
yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI 381
                                                                                                                                                                                                                                                                       431 lySerLysTrpMetTyrValGlyArgGlnAsnAlaGlyGlnThrTrpThr 447
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                                                                                           AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
                                  TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
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66.460
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227 c 352 a
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Sequence 15 from patent
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AR129918.1 GI:14117815
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Percent Similarity: 89.027
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US-09-590-375-1 x AR129918
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LOCUS AR129918
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56

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17

source

BASE COUNT

ORIGIN

DEFINITION

464

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

FEATURES

nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA 34

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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
                                                                                                                                                                                                        ValValMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
                                                                                                                                                                                                                                                                aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT 134
                                                                                                                                                                                                                                                                                                                                                                       hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nArgTyrGln...GluAsnHisIlePheArgPheAlaAsnThrAsn.... 181
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                                                              GlnAlaAspValGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh
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ATGGGGAGAATGGTATACAATACATTAAATCTTGATGGATTTAGGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

I (bases 1 to 1455)
Svendsen,A., Wijacrulff,S., Bisgaard-Frantzen,H. and Andersen,C..
alpha.-Amylase variants
Patent: US 6197565-A 10 06-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-2001
                                                                                                                                                                                                                                                 1306
                                                                                                                                                   1057 TATGCGCTTATTTTAACAAGAGAACAAGGCTATCCCTCTGTCTTTTATGG 1106
                                                                                                                                                                                                                             431
          347
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       yAspTyrTyrGlylleProAsnAspAsnIleSerAlaLysLysAspMetI
                                                                                                         AspTyrPheAspHisTrpAspValValGlyTrpThrArgGluGlySerSe
                                                                                                                                                                                                                            414 rSerArgProAsnSerGlyLeuAlaThrIleMetSerAsnGlyProGlyG
                                                   TyrAlaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
                                                                                                                                       leAspGluLeuLeuAspAlaArgGlnAsnTyrAlaTyrGlyThrGlnHis
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2
66.460
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Identity:
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227 c 352 g
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US (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent
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Ratio: 4.327
nilarity: 89.027
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US-09-590-375-1 x AR137884
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LOCUS AR137884
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VERSION
KEYWORDS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
         331
                             1001
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hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAlaTyr 150
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                                 84 luargalaileGlySerLeuLysSerAsnAspileAsnValTyrGlyAsp 100
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256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP 331
                                                                                    67
                                                                                                                                      84
                                                                                 AGTCTGCCATCCATGCTTTAAAGAATAATGGCGTTCAAGTTTATGGGGAT
                                                                                                                                                                                                                                                                                            aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu
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                                                                                                                                      eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
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364

398 1207

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7 AATGGGACAAATGGGACGATGATGCAATACTTTGAATGGCACTTGCCTAA
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Svendsen, A., Kjaerulff, S., Bisgaard-Frantzen, H. and Andersen, C.
alpha. Amylase variants
Patent: US 6197565-A 14 06-WAR-2001;
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                                                                                                 1057 TATGCGCTTATTTAACAAGAACAAGGCTATCCCTCTGTCTTCTATGG
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                                                                                                                                     yAspTyrTyrGlylleProAsnAspAsnIleSerAlaLysLysAspMetI
                                     roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                    348 TyralaThrIleLeuThrArgGluGlyGlyTyrProAsnValPheTyrGl
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Percent Identity: 66.460
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LOCUS AR137888 1455 bp DNA
DEFINITION Sequence 14 from patent US 6197565.
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1. .1455
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227 c 352 a
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Ratio: 4.327
Harity: 89.027
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US-09-590-375-1 x AR137888
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1357

1407

source

FEATURES TITLE

AUTHORS JOURNAL

REFERENCE

BASE COUNT

ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
                ValvalMetAsnHisLysMetGlyAlaAspPheThrGluAlaValGlnAl 117
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nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA
                                                 {\tt GlnAlaAspValGlyAlaTyrAspLeuTyrAspLeuGlyGluPh}
                                                                                                                                                          eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
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657 ATGGGAGATGTATACAATACATTAAATCTTGATGGATTTAGGATCG
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Borchert,T.Vedel, Svendsen,A., Andersen,C., Nielsen,B., Nissen,T.Lauesgaard and Kj.ae butted.rulff,Sslashedren.alpha.amlase mutants
Patent: US 6204232-A 10 20 WAR-2001;
Location/Qualifiers
1. .1455
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1007 CTGGGGAATCATTAGAATCATTTGTACAAGAATGGTTTAAGCCACTTGCT
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                                              roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
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227 c 352 q
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AR143214
AR143214.1 GI:15104500
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US-09-590-375-1 x AR143214
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US-09-590-375-1 x AR143218

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08-AUG-2001
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1 (bases 1 to 1455)

1 (bases 1 to 1455)

Borchert, T.Vedel, Svendsen, A., Andersen, C., Nielsen, B., Nissen, T.Leuesgaard and Kjae butted.rulff, Sslashedren.alpha.amlase mutants
Patent: US 6204232-A 14 20-WAR-2001;
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             GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
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Percent Identity: 66.460
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LOCUS ARM43218 1455 bp DNA
LOCUS Sequence 14 from patent US 6204232.
ACCESSION ARM43218
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1. .1455
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227 c 352 g
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VERSION
KEYWORDS
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84 luArgAlaIleGlySerLeuLysSerAsnAspIleAsnValTyrGlyAsp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnArgAsnGluAlaAspGlnAspLeuPheValValGlyGluTyrTrpLy 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAAGAAACGCAACGGGAAAAGAAATGTTTGCTGTTGCTGAATTTTGGAA 806
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                           1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs
                                                     nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaAlaLeuSerA
                                                                                                                                                                 eAsnGlnLysGlyThrValArgThrLysTyrGlyThrLysAlaGlnLeuG
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  to: 1455
 from: 1
to: AR143218
Align seg 1/1
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1. .144
145. .1695
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amylass from
Bacillus sp.'
1696. .1776
re 1. .31
/note='Slonal sequences'
re 127. .132
re 127. .132
9. .14
95. .100
31. .366
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Percent Identity: 66.874
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/organism="Bacillus sp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 1776
                                                                                                                                                                                                                                                             signal 120. .125 Location/Qualifiers
                                                                                                                                                                                                                                                                                                            /db_xref="taxon:1409"
305 c 417 g
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 topology: Linear;
hypothetical: No;
anti-sense: No;
                                                                                                                                                                              misc_feature
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Percent Similarity: 89.234
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LOCUS E12445 1776 bp DNA PAT 24-JUN-1998
DEFINITION DNA encoding liquefaction type alkaline alpha amylase from Bacillus
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HATADA YUUJI, OZAKI KATSUYA, ARA KATSUTOSHI, KAWAI SHUJI,
                                                                                                                                                                         1206
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                                                                                                                                                                                                                                                                                                                                                                              GAGAGAAATGGATGTACGTAGGGCAAAATAAAGCAGGTCAAGTTTGGCAT 1356
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E12445.
E12445.
G1:3251278
B2F1196336392-A/1.
Bacillus sp.
Bacillus sp.
Bacillus sp.
Bacillus sp.
Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                Ito,S.
                                                                                 314 uAlaHisProMetHisAlaValThrPheValAspAsnHisAspThrGlnP
                                                                                                                                           roGlyGluSerLeuGluSerTrpValAlaAspTrpPheLysProLeuAla
                                                                                                                                                                                                                           364 yAspTyrTyrGlyIleProAsnAspAsnIleSerAlaLysLysAspMetI
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                                  GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
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LIQUEFIED-TYPE ALKALI ALPHA-AMYLASE GENE
PATENT: JP 1996336392-A 1 24-DEC-1996;
KAO CORP
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strandedness: Double;
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JP 1996336392-A/1
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994 GIGCGIAACACCACAGGIAAACCAAIGITIGCAGIIGCAGAAITITIGGAA 1043
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                                                                                                                   ..TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu 197
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hrIleAspAlaTrpThrGlyPheAspPheSerGlyArgAsnAsnAlaTyr 150
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                         n...ArgTyrGlnGluAsnHisIlePheArgPheAlaAsnThrAsn...
                                                                                          SerAspPheLysTrpArgTrpPheHisPheAsnGlyValAspTrpAspGl
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Igarashi,K., Hatada,Y., Ikawa,K., Araki,H., Ozawa,T., Kobayashi,T., Ozaki,K. and Ito,S.
Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding Bliochem. Blophys. Res. Commun. 248 (2), 372-377 (1998)
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SHPNSGLATIMSDGFGGNKWMYVGKHKAGQVWRDITGNRSGTVTINADGWGNFTVNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-NOV-1997) to the DDBJ/EMBL/GenBank databases. Yuji
Hatada, Kao Corporation, Tochigi Research Laboratories; 2606
Akabane, Ichikai, Haga-gun, Tochigi 321-3497, Japan
(Tel:0285-68-7400, Fax:0285-68-7403)
                                                                                                                                                                                                                                                                                                    21-AUG-1998
                                                                         GTAATAAATGGATGTATGTCGGGAAACATAAAGCTGGCCAAGTATGGAGA 1593
                                             AspLeuThrGlyAsnAsnGlyAlaSerValThrIleAsnGlyAspGlyTr 464
                                                                                                                                                               464 pGlyGluPhePheThrAsnGlyGlySerValSerValTyrValAsnGln 480
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1 (bases 1 to 1786)
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Bacillus sp. gene for amylase, complete cds.
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Bacillus sp.
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/product="amylase"
/protein_id="BAA32431.1"
/db_xref="G1:3445480"
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155. .1705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
```

1 AspGlyLeuAsnGlyThrMetMetGlnTyrTyrGluTrpHisLeuGluAs 17

303	34 353	50 403	67 453	84. 503.	100 553	117	134 653	150	167 753	181 803	197 853	214 903	231 953	247 1003	264 1053	281 1103	297 1153	314
:::	nAspGlyGlnHisTrpAsnArgLeuHisAspAspAlaAlaLeuSerA 	spalaglylleThralalleTrplleProProAlaTyrLysGlyAsnSer :: ::	GInalaaspvalGlyTyrGlyAlaTyrAspLeuTyrAspLeuGlyGluPh 	eAsnGlnLysGlyThrValargThrLysTyrGlyThrLysAlaGlnLeuG 	luargalaileGlySerLeuLysSerAsnaspIleAsnValTyrGlyAsp :: :::	ValvalmetasnHisLysMetGlyalaaspPheThrGlualaValGlnal 	aValGlnValAsnProThrAsnArgTrpGlnAspIleSerGlyAlaTyrT ::: :::	hrileaspalatrpthrGlyPheaspPheSerGlyArgAsnasnalaTyr ::	SeraspPheLysTrpArgTrpPheHisPheAsnGlyValaspTrpAspGl :::	nArgTyrG] GTCACGTCAGCI	TrpAsnTrpArgValAspGluGluAsnGlyAsnTyrAspTyrLeuLeu ::: :::	GlySerAsnile :::::: TATGCAGACATI	<pre>pTrpGlySerTrpPheThrAspGluLeuAspLeuAspGlyTyrArgLeuA : :: :: TrGGGAGTTTGGTATACAAATACACTTAATCTAGATGGATTTAGAATGG</pre>	spalailelyshisileprophetrptyrthiserasptrpvalarghis ::: ::	GlnArgAsr GTGCGTAAC	SASPASPVAIGIYAIALEUGIUPheTyrLeuAspGluMetAsnTrpGluM ::: ::: ::: AAATGACCTTGCTGCAATCGAAACTATTTAAATAAAAGAAGTTGGAATC	etSerLeupheAspValProLeuAsnTyrAsnPheTyrArgAlaSerGln :::	GlnGlyGlySerTyrAspMetArgAsnIleLeuArgGlySerLeuValGl
254	1 7 304	34 354	51	67 454	84 504	101 554	117 604	134 654	151 704	167 754	182 804	198 854	214 904	231 954	248	264 .054	281 .104	298

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